

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 19:50:27 ; Search time 2978 Seconds
(without alignments)
11150.538 Million cell updates/sec

Title: US-09-617-174c-1
Perfect score: 1141
Sequence: 1 agataagcacagcagagaag.....aggataactgtgactccagg 1141

Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

- 1: gb_ba.*
- 2: gb_hvg.*
- 3: gb_in.*
- 4: gb_om.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_scs.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vl.*
- 15: em_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_mu.*
- 20: em_om.*
- 21: em_or.*
- 22: em_ov.*
- 23: em_pat.*
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- 25: em_pl.*
- 26: em_ro.*
- 27: em_scs.*
- 28: em_un.*
- 29: em_vl.*
- 30: em_hvg_hum.*
- 31: em_hvg_inv.*
- 32: em_hvg_other.*
- 33: em_hvg_mus.*
- 34: em_hvg_pln.*
- 35: em_hvg_rod.*
- 36: em_hvg_mam.*
- 37: em_hvg_vrt.*
- 38: em_sy.*
- 39: em_higo_hum.*
- 40: em_higo_mus.*
- 41: em_higo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1129.8	99.0	170269	9	AC090307	AC090307 Homo sapi
C 2	1129.8	99.0	173252	9	AC036176	AC036176 Homo sapi
C 3	1129.8	99.0	173836	2	AP001404	AP001404 Homo sapi
C 4	745.4	65.3	12426	6	AX251236	AX251236 Sequence
C 5	723.4	63.4	12426	6	AX251235	AX251235 Sequence
C 6	612	53.6	214212	2	AC015793	AC015793 Homo sapi
C 7	437.6	38.4	214212	2	AC015793	AC015793 Homo sapi
C 8	203.4	17.8	44255	9	AL356309	AL356309 Human DNA
C 9	199.4	17.5	84577	9	AC079927	AC079927 Homo sapi
C 10	196.6	17.2	143721	9	AC117414	AC117414 Homo sapi
C 11	195	17.1	2343	9	AK023951	AK023951 Homo sapi
C 12	195	17.1	71872	9	AL133390	AL133390 Human DNA
C 13	195	17.1	147259	2	AC019248	AC019248 Homo sapi
C 14	195	17.1	184703	9	AL365215	AL365215 Human DNA
C 15	194	17.0	164167	2	AC090104	AC090104 Homo sapi
C 16	194	17.0	189018	9	AC091185	AC091185 Homo sapi
C 17	193.4	17.0	158806	2	AL591132	AL591132 Homo sapi
C 18	193.4	17.0	168834	2	AL355583	AL355583 Homo sapi
C 19	193.4	17.0	197864	9	HSY214810	AL022344 Human DNA
C 20	193.4	17.0	200882	2	AL591181	AL591181 Homo sapi
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C 28	191.6	16.8	15614	2	AC012620	AC012620 Homo sapi
C 29	191.6	16.8	160883	9	AC021498	AC021498 Homo sapi
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C 34	190.8	16.7	102837	9	HS22202	295329 Human DNA s
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ALIGNMENTS

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DEFINITION Homo sapiens chromosome 18, clone RP11-851B10, complete sequence.
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VERSION AC090307.7 GI:16041402
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Sukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 170269)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 18, clone RP11-851B10
JOURNAL Unpublished

2 (bases 1 to 170269)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Boguslavsky,L., Bouckgalter,B., Brown,A.,
 Camarata,J., Campopiano,A., Choepel,J., Colangelo,M., Collins,S.,
 Collamore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S.,
 Dodge,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J.,
 Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,
 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
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 Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,
 O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,
 Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R.,
 Riback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,
 Roy,A., Santos,R., Schauer,S., Schupbach,R., Seaman,S., Severy,P.,
 Sounges,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
 Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
 Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
 Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 170269)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
 Anderson,S., Barna,N., Bastien,V., Boguslavsky,L., Bouckgalter,B.,
 Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,
 Choepel,Y., Colangelo,M., Collins,S., Collamore,A., Cook,A.,
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 Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
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 Hagos,B., Heaford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,
 Jones,C., Karatas,A., Karatas,A., Kells,C., LaRocque,K.,
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 Maclean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C.,
 McCarthy,M., McEwan,P., McKernan,K., McPheeters,R., Meldrim,J.,
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 Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
 Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V.,
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 Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
 Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (30-DEC-2001) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Oct 11, 2001 this sequence version replaced gi:15290867.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center.
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L12576
 Center clone name: 851_B_10

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Tue Jun 10 08:56:17 2003

On Mar 19, 2002 this sequence version replaced gi:17647019.

All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: http://www-seq.wi.mit.edu

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: L9215

Center clone name: 635_N_19

FEATURES

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COMMENT

Campiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S.,
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 Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
 Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,
 Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
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 Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J.,
 Levine, R., Liu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,
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 Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Olivari, T.M., Oliver, J., Peterson, K., Pierre, N.,
 Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
 Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission

Submitted (07-APR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 173252)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
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 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (19-MAR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (bases 1 to 173252)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
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 Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
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 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission

Submitted (22-MAR-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA

TITLE
JOURNALTITLE
JOURNALREFERENCE
AUTHORSREFERENCE
AUTHORS

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repeat_region /rpt_family="(ATG)n"
repeat_region complement(17753..17944)
repeat_region /rpt_family="MER91A"
repeat_region 18683..18982
repeat_region /rpt_family="AluY"
repeat_region complement(19042..19306)
repeat_region /rpt_family="AluSx"
repeat_region complement(19307..19393)
repeat_region /rpt_family="MER103"
repeat_region complement(20344..20790)
repeat_region /rpt_family="L1M4A"
repeat_region 20818..21042

Query Match 99.0%; Score 1129.8; DB 9; Length 173252;
Best Local Similarity 99.4%; Pred. No. 4.5e-308;
Matches 1134; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AGATAAGCAGCAGAGAGACCAACGCTCCGTTTCAGGTCCTTTCTGAGGCTGATTCG 60
DB 52817 AGATAAGCAGCAGAGAGACCAACGCTCCGTTTCAGGTCCTTTCTGAGGCTGATTCG 52758

QY 61 GCTGGAAGGAGTAGTCCACCAATGAAGAGCTGCGGAGAGCAGGAGGACAGAAC 120
DB 52757 GCTGGAAGGAGTAGTCCGCGCAATGAAGAGCTGCGGAGAGCAGGAGGACAGAAC 52698

QY 121 AGGCTCCAGAGAGATTTTCAGAGCAGAGCTGCTACTCTCTTTCTTTTCTTTTCTTTT 180
DB 52697 AGGCTCCAGAGAGATTTTCAGAGCAGAGCTGCTACTCTCTTTCTTTTCTTTTCTTTT 52638

QY 181 GCTCTGTACCCAGGCTGAAGTACAGTGTAGCTCACGGCTCACTGCAAGCTTGACCTC 240
DB 52637 GCTCTGTACCCAGGCTGAAGTACAGTGTAGCTCACGGCTCACTGCAAGCTTGACCTC 52578

QY 241 CCAGGCTCAAGTATCTCTCTGCTCAGCTTTCAGTAACTGCGGACCAAGCATGCAT 300
DB 52577 CCAGGCTCAAGTATCTCTCTGCTCAGCTTTCAGTAACTGCGGACCAAGCATGCAT 52518

QY 301 CACCAGCTAGGCTATGTTTATACATTTTGTAGAGATGGGCTCTCACCATGTTGCCCA 360
DB 52517 CACCAGCTAGGCTATGTTTATACATTTTGTAGAGATGGGCTCTCACCATGTTGCCCA 52458

QY 361 GGTGTGTCTCAAACTCCTGGGCTCAAGCAATCCGCTCAGCTCAACTCCCCAAAGCTCG 420
DB 52457 GGTGTGTCTCAAACTCCTGGGCTCAAGCAATCCGCTCAGCTCAACTCCCCAAAGCTCG 52398

QY 421 GATTACAGGCTGAGCCAGCGGCTGAGTAACTCTATACAGGATTTTAAAAA 480
DB 52397 GATTACAGGCTGAGCCAGCGGCTGAGTAACTCTATACAGGATTTTAAAAA 52338

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QY 481 GAAACTTCTGCGCCACCAATTAACCAATATCTCTACCAATTTGCTAGTAATATTTTG 540
DB 52337 GAAACTTCTGCGCCACCAATTAACCAATATCTCTACCAATTTGCTAGTAATATTTTG 52278

QY 541 CTAATAGTACCTAAATTTTAGTAGGCACCTGTGTTATACATATATCCATCTCTCTTT 600
DB 52277 CTAATAGTACCTAAATTTTAGTAGGCACCTGTGTTATACATATATCCATCTCTTT 52218

QY 601 TTGATTGCTCTTCTGTTTAAATGGCAGCTACCTCTCTGGCATCTAGCAGAAATGAGCTGC 660
DB 52217 TTGATTGCTCTTCTGTTTAAATGGCAGCTACCTCTCTGGCATCTAGCAGAAATGAGCTGC 52158

QY 661 TGCAGTTTACACAAAAGAAATGGAGATCAGAGTACTTTTTTGTGCCACCAACCTGTCTGAG 720
DB 52157 TGCAGTTTACACAAAAGAAATGGAGATCAGAGTACTTTTTTGTGCCACCAACCTGTCTGAG 52098

QY 721 AAATTTGTAGTGTACTATCATCATCATCTATTTTATTTTATCGAATATTTTACCTTCC 780
DB 52097 AAATTTGTAGTGTACTATCATCATCATCTATTTTATTTTATCGAATATTTTACCTTCC 52038

QY 781 GGTCTCTGCGTGGCGGAGAGGATTCGCTACCATGCTCTGTAGTATGATGTAATCTCAC 840
DB 52037 GGTCTCTGCGTGGCGGAGAGGATTCGCTACCATGCTCTGTAGTATGATGTAATCTCAC 51978

QY 841 AGCCCCCTTCTGCTCCGCAACATGTTGGAGGCTTTTGGAAAGCTGTGCAGACCAACAGCAACT 900
DB 51977 AGCCCCCTTCTGCTCCGCAACATGTTGGAGGCTTTTGGAAAGCTGTGCAGACCAACAGCAACT 51918

QY 901 TCAGCTCGAATCATCTCTTTTCAATTTGTGCAAGCTGCCAAGAGGCTTGAGTAGGAGAGG 960
DB 51917 TCAGCTCGAATCATCTCTTTTCAATTTGTGCAAGCTGCCAAGAGGCTTGAGTAGGAGAGG 51858

QY 961 AGTGGCGCGAGCGCGGCGGCGGCTGAGCTGGCTGGCAGTGGCGGTGGCGGT 1020
DB 51857 AGTGGCGCGAGCGCGGCGGCGGCTGAGCTGGCTGGCAGTGGCGGTGGCGGT 51798

QY 1021 GCTGCCAGGTGAGCCACCGCTGCTTCTGCCAGACACCGTGGCTTCCATCTCCAGGTCT 1080
DB 51797 GCTGCCAGGTGAGCCACCGCTGCTTCTGCCAGACACCGTGGCTTCCATCTCCAGGTCT 51738

QY 1081 TTGTGCTCTCGCTGCTGCTGCTTCTTTTCCAGCATTTTCCAGGATAAATGTGACTCCAG 1140
DB 51737 TTGTGCTCTCGCTGCTGCTTCTTTTCCAGCATTTTCCAGGATAAATGTGACTCCAG 51678

QY 1141 G 1141
DB 51677 G 51677

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RESULT 3

AP001404/c

LOCUS

DEFINITION

AP001404

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AP001404 Homo sapiens chromosome 18 clone RP11-851B10 map 18q22, WORKING DRAFT SEQUENCE, 11 unordered pieces.

AP001404.3 GI:9188495 HTG; HTGS_PHASE1; HTGS_DRAFT.

Homo sapiens DNA, HOMO sapiens

REFERENCE 1 (bases 1 to 173336) Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Published Only in DataBase (2000)

REFERENCE 2 (bases 1 to 173836) Hattori, M., Ishii, K., Toyoda, A., Taylor, T. D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission

Submitted (14-MAR-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

COMMENT

Query Match	99.0%	Score 1129.8	DB 2	Length 173836
Best Local Similarity	99.4%	Pred. No. 4.5e-308		
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61	GCTGGAAGGGAGTAGGTCCTCCACCAATATGAGAAGCTGTGGAGACAGGAGGACAAAGAAC	120		
150664	GCTGGAAGGGAGTAGGTCCTCCCAATATGAGAAGCTGTGGAGACAGGAGGACAAAGAAC	150605		
121	AGGCTCCACGAAGAGATTTACAGACGAGCTGCGTATCTCTTTTCTTTTGTGTTCTTTT	180		
150604	AGGCTCCACGAAGAGATTTACAGACGAGCTGCGTATCTCTTTTCTTTTGTGTTCTTTT	150545		
181	GCTCTGTACCCAGGCTCAAGTACAGTGGTTAGTCTACGGCTCACTGCAGCTTTGACCTC	240		
150544	GCTCTGTACCCAGGCTCAAGTACAGTGGTTAGTCTACGGCTCACTGCAGCTTTGACCTC	150485		
241	CCAGGCTCAAGTGATCTCTCGTCTCAGCTTTTCCAAGTAATCTGGGACACAGGCAATGCAT	300		
150484	CCAGGCTCAAGTGATCTCTCGTCTCAGCTTTTCCAAGTAATCTGGGACACAGGCAATGCAT	150425		
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361	GGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGCTCAAACTCCCCAAATGCTGG	420		
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421	GATTACAGGCGTGAGCCACCGGCCACGGGCTGAGTAATCTCTAATCACAGGATTTTAAAAA	480		
150304	GATTACAGGCGTGAGCCACCGGCCACGGGCTGAGTAATCTCTAATCACAGGATTTTAAAAA	150245		
481	GAAACTTCCTGGCCACCCATTAAACAATATCTCTACCAATTCGTTAGTAATAATTTTG	540		
150244	GAAACTTCCTGGCCACCCATTAAACAATATCTCTACCAATTCGTTAGTAATAATTTTG	150185		
541	CTAATAGTACTAATTTTATAGGTAGGCACTGTGTTTATACATATATCCATTCTCTTTT	600		
150184	CTAATAGTACTAATTTTATAGGTAGGCACTGTGTTTATACATATATCCATTCTCTTTT	150125		
601	TTGATTGCTCTTCTGTTTAAATGGGAGCTACCTCTCTTGGCATCTAGCAGATGAGCTGC	660		

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[illegible]

4581	DB	GTAGTTTATATAAAAAAGATTAGAGATTAGAGTATTTTTGTGTTATTAACGTTGTTGAG	4640
721	QY	AAATTTGTAGTGTACTATCATCACATTAACCTTTATTTTCATCGATATTTTTCACCTTCC	780
4641	DB	AAATTTGTAGTGTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTTTC	4700
781	QY	GGTCCTCGGTGGCCGAGAGGATCCGGTACGCATGCTGTACGTATGCATGTAACCTCAC	840
4701	DB	GGTTTGGCGTGGTCCGAGAGGATTCGTGTCGTATGTTTGTACGTATGTTATGTAATTTAT	4760
841	QY	AGCCCTTCTCTGCCCAACATGTTGGAGGCTTTTGGAAAGCTGTGCAGACAACACGCAACT	900
4761	DB	AGTTTGTGTTGTCGAAATATGTTGGAGGTTTGTGGAGTTGTTGGAGTTGTTAGTAATAAGTAAT	4820
901	QY	TCAGCTCGAATCATCTCTTTTCAATTGTGGCAAGCTGCCAAGAGCTTGTAGTAGGAGG	960
4821	DB	TTAGTTTGAATATTTTTTTTTTAAATGCGATAGTGTAAAGAGGTTTGAGTAGGAGG	4880
961	QY	AGTCCCGCAGAGCGGGCGGGCGGTGCGAGCTGGCGTGGCAGTGGCGGTGGCGGT	1020
4881	DB	AGTGTGTCGAGCGGGCGGGCGGGCGGTGCGAGTTGGGTTGGTAGTGGCGGTGGCGGT	4940
1021	QY	GCTGCCAGGTGAGCACACCCTCTCTCTGCCCAGACAGGTCCGCTCCACATCCAGTCT	1080
4941	DB	GTGTTGTTAGTGAATATCGTTGTTTGTGTTAGATACGTCGTTTATATTTAGTGT	5000
1081	QY	TGTGTCCTCGCTTGGCTGTTCTTTTCCACGCATTTTCCAGGATAACTGTGACTCCAG	1140
5001	DB	TTGTGTTTTCGTTTGTGTTTGTGTTTTTTTACGATATTTTTTAGGATATTTGATTTAG	5060
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5061	DB	G 5061	

RESULT 6	AC015793/c
LOCUS	214212 bp DNA linear HTG 13-JUL-2000
DEFINITION	Homo sapiens chromosome 18 clone RP11-1117D15 map 18, LOW-PASS SEQUENCE SMPLEING.
ACCESSION	AC015793
VERSION	AC015793.2 GI:7144769
KEYWORDS	HTG; HTGS, PHASE0.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1. (bases 1 to 214212)
TITLE	Birren, B., Linton, L., Nusbaum, C. and Lander, E.
JOURNAL	Homo sapiens chromosome 18, clone RP11-1117D15
REFERENCE	2. (bases 1 to 214212)
AUTHORS	Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavsky, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArelzano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Grant, G., Hagos, B., Kann, L., Karatas, A., Klein, J., Howland, J., Gardyna, S., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lechoczky, J., Lieu, C., Locks, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Navlor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Teyfay, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
TITLE	Direct Submission
JOURNAL	Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT	On Mar 3, 2000 this sequence version replaced gi:6446894. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RN/RepeatMasker.html

AX251235	LOCUS	AX251235	12426 bp	DNA	linear	PAT 05-OCT-2001
DEFINITION	Sequence 203 from Patent WO0168912.					
ACCESSION	AX251235					
VERSION	AX251235.1	GI:15984658				
KEYWORDS	synthetic construct.					
ORGANISM	synthetic construct					
REFERENCE	artificial sequences					
AUTHORS	1 (bases 1 to 12426)					
TITLE	Olek, A., Piepenbrock, C. and Berlin, K.					
JOURNAL	Diagnosis of diseases associated with tumor suppressor genes and oncogenes					
FEATURES	Patent: WO 0168912-A 203 20-SEP-2001;					
source	Epigenomics AG (DE)					
BASE COUNT	3527 a 137 c 2591 g 6171 t					
ORIGIN	Location/Qualifiers					
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	/db_xref="taxon:32630"					
	/note="chemically treated genomic DNA (Homo sapiens)"					
Query Match	63.4%; Score 723.4; DB 6; Length 12426;					
Best Local Similarity	77.1%; Pred No. 2.4e-193;					
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QY	1 AGATAAGCACACGACGAGAGCAAC	CAGCTCCGTTTCAGTCTCTTCTCGAGGCTGATTCG	60			
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Db	3981 GTTGGAGGGGTAGGTTTCGTT	AAATGAGAGTGTGGAGAGATAGGAGGATAAGAAT	4040			
QY	121 AGGCTCCAGCAAGAGANTT	CAGCAGAGCTCGGTACTCTTTTCTTTTCTTTCTTTT	180			
Db	4041 AGGTTTTACGAAGAGATT	TTAGAGTAGAGTTCCGTAATTTTTTTTTTTTTTTTTTT	4100			
QY	181 GCTCTGTCACCCAGGCTGAAG	TACAGTGGTTAGCTCACGGCTCACTGCAGAGCTTTGACCTC	240			
Db	4101 GTTTTGTGTAATTTAGGTTGA	AGATATAGTGGTTATTCGGTTTATTTAGTTTGTGATTTT	4160			
QY	241 CCAAGGCTCAAGTGATCCTCT	CGTCTCAGCTTTCCAAAGTAACTGGGACACACAGGCATGAT	300			
Db	4161 TTAGGTTTAAGTGATTTT	TCGTTTTCGTTTAAAGTAAATTTGGGATATATAGGTATGTAT	4220			
QY	301 CACACGCTAGGCTATGTTT	TATGTTTACATTTTTTGTAGAGATGGGGTCTCACCATGTTGCCCA	360			
Db	4221 TATTATATATAGGTTATGTT	TATATATTTTTTTGTAGAGATGGGGTTTATATGTTGTTTA	4280			
QY	361 GGTGTGCTCAAACTCCTCGG	CTCAAGCAATCGCTCACTCACTCCCAAAATGCTGG	420			
Db	4281 GGTGTGTTTAAATTTTT	TGGGTTTAAAGTAATTCGTTTAAATTTTTTAAATGTTGG	4340			
QY	421 GATTACAGGCGTGAGCCAC	CGGCCAGGCTGAGTAATCCTAATACAGGATTTTAAAAA	480			
Db	4341 GATTATAGGCGTGAGTTAT	CGCGTTAGGTTGAGTAATTTTAAATATAGGATTTAAAAA	4400			
QY	481 GAAACTTCTCGGCCACCCAT	TAAACAATATCTCTACCAATTTGGTGTAGTAATATTTTG	540			
Db	4401 GAAATTTTTCGGTTATT	TATTAATAATAATTTTTTAAATTTTAAATTTGGTAGTAATAATTTG	4460			
QY	541 CTAATAGTACCTAATTTTT	TAGTAGGACCTGCTGTTTATACATATCCATTCCTCTTT	600			
Db	4461 TTAATAGTATTTAAATTT	TAGTAGGATTTGTTTATATATATATATTTTTTTTTTTT	4520			
QY	601 TTGATTGCTTTCTGTTTAA	TGGGCGAGCTACCTCTCTTGGCACTACGAAATGAGCTGC	660			
Db	4521 TTGATTGTTTTTTGTTTAA	TGGGTAGTATTTTTTTTTTGGTATTTTATAGTAATGAGTTGT	4580			
QY	661 TGCAGTTTACAAAAAGAA	TGGAGATCAGAGTACTTTTTGTGCCACCAACGCTGCTGAG	720			

----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L1590
 Center clone name: L117_D_15

* NOTE: This record contains 240 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

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 * 2338 2437: gap of 100 bp
 * 2438 3161: contig of 724 bp in length
 * 3162 3261: gap of 100 bp
 * 3262 3966: contig of 705 bp in length
 * 3967 4066: gap of 100 bp
 * 4067 4772: contig of 706 bp in length
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 * 8029 8128: gap of 100 bp
 * 8129 8803: contig of 675 bp in length
 * 8804 8903: gap of 100 bp
 * 8904 9613: contig of 710 bp in length
 * 9614 9713: gap of 100 bp
 * 9714 10409: contig of 696 bp in length
 * 10410 10509: gap of 100 bp
 * 10510 11237: contig of 728 bp in length
 * 11238 11337: gap of 100 bp
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 * 12044 12143: gap of 100 bp
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 * 12968 13660: contig of 693 bp in length
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[illegible]

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 * 30018 30724: contig of 707 bp in length
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 * 30825 31529: contig of 705 bp in length
 * 31530 31629: gap of 100 bp
 * 31630 32324: contig of 695 bp in length
 * 32325 32424: gap of 100 bp
 * 32425 33116: contig of 692 bp in length
 * 33117 33216: gap of 100 bp
 * 33217 33936: contig of 720 bp in length
 * 33937 34036: gap of 100 bp
 * 34037 34750: contig of 714 bp in length

* 34751 34850: gap of 100 bp
 * 34851 35578: contig of 728 bp in length
 * 35579 35678: gap of 100 bp
 * 35679 36393: contig of 715 bp in length
 * 36394 36493: gap of 100 bp
 * 36494 37203: contig of 710 bp in length
 * 37204 37303: gap of 100 bp
 * 37304 37965: contig of 662 bp in length
 * 37966 38065: gap of 100 bp
 * 38066 38781: contig of 716 bp in length
 * 38782 38881: gap of 100 bp
 * 38882 39590: contig of 709 bp in length
 * 39591 39690: gap of 100 bp
 * 39691 40403: contig of 713 bp in length
 * 40404 40503: gap of 100 bp
 * 40504 41238: contig of 735 bp in length
 * 41239 41338: gap of 100 bp
 * 41339 42054: contig of 726 bp in length
 * 42055 42164: gap of 100 bp
 * 42165 42880: contig of 716 bp in length
 * 42881 42980: gap of 100 bp
 * 42981 43687: contig of 707 bp in length
 * 43688 43787: gap of 100 bp
 * 43788 44504: contig of 717 bp in length
 * 44505 44604: gap of 100 bp
 * 44605 45307: contig of 703 bp in length
 * 45308 45407: gap of 100 bp
 * 45408 46106: contig of 699 bp in length
 * 46107 46206: gap of 100 bp
 * 46207 46909: contig of 703 bp in length
 * 46910 47009: gap of 100 bp
 * 47010 47696: contig of 687 bp in length
 * 47697 47796: gap of 100 bp
 * 47797 48511: contig of 735 bp in length
 * 48512 48631: gap of 100 bp
 * 48632 49341: contig of 710 bp in length
 * 49342 49441: gap of 100 bp
 * 49442 50162: contig of 721 bp in length
 * 50163 50262: gap of 100 bp
 * 50263 50990: contig of 728 bp in length
 * 50991 51090: gap of 100 bp
 * 51091 51803: contig of 713 bp in length
 * 51804 51903: gap of 100 bp
 * 51904 52610: contig of 707 bp in length
 * 52611 52710: gap of 100 bp
 * 52711 53412: contig of 702 bp in length
 * 53413 53512: gap of 100 bp
 * 53513 54253: contig of 741 bp in length
 * 54254 54353: gap of 100 bp
 * 54354 55084: contig of 731 bp in length
 * 55085 55184: gap of 100 bp
 * 55185 55972: contig of 788 bp in length
 * 55973 56072: gap of 100 bp
 * 56073 56855: contig of 783 bp in length
 * 56856 56955: gap of 100 bp
 * 56956 57708: contig of 753 bp in length
 * 57709 57808: gap of 100 bp
 * 57809 58579: contig of 771 bp in length
 * 58580 58679: gap of 100 bp

Query Match 38.4%; Score 437.6; DB 2; Length 214212;
 Best Local Similarity 78.7%; Pred. No. 4e-112;
 Matches 463; Conservative 0; Mismatches 124; Indels 1; Gaps 1;

QY 1 AGATAAGCACACAGACAGAGCAACAGCTCCCTTTTCAGGTCCTTTCTCAGGCTGATTTCG 60
 |||||
 DB 7551 AGATAAGCACACAGACAGAGCAACAGCTCCCTTTTCAGGTCCTTTCTCAGGCTGATTTCG 7610
 |||||
 QY 61 GCTGGAAGGGAGTAGTCCCAACCAATGAAGAGCTGTGGGAGACAGACGACCAAGAAC 120
 |||||
 DB 7611 GCTGGAAGGGAGTAGTCCCGCCCAATGAAGAGCTGTGGGAGACAGACGACCAAGAAC 7670
 |||||
 QY 121 AGGCTCCACGAAGAGATTTTCAGAGCAGAGCTCGTACTCTTTTCTTTTCTTTTCTTTT 180

Db 7671 ACCTCCAGGAGATTTTCAGAGCAGAGCTGCGTACTCTCTTTTCTTTTCTTTTCTTTT 7730

QY 181 GCTCTGTACCCAGGCTGAGTACAGTGGTGTAGCTCAGGCTCAGCTGAGCTTTGACCTC 240

Db 7731 GCTCTGTACCCAGGCTGAGTACAGTGGTGTAGCTCAGGCTCAGCTGAGCTTTGACCTC 7790

QY 241 CCAGGCTCAAGTGATCTCTGCTCAGCTTTTCCAGTAACTGGGACACACAGGCTGAT 300

Db 7791 CCAGGCTCAAGTGATCTCTGCTCAGCTTTTCCAGTAACTGGGACACACAGGCTGAT 7850

QY 301 CACCAGCTAGGCTATGTTTACATTTTGTAGAGATGGGCTCTCACCATTGTGCCA 360

Db 7851 CACCAGCTATGCTATGTTTACATTTTGTAGAGATGGGCTCTCACCATTGTGCCA 7910

QY 361 GGTGTGTCAAACTCCTGGGCTCAAGCAATCGCTCAGCTCAAACTCCTCCCAATGCTGG 420

Db 7911 GGTGTGTCAAACTCCTGGGCTCAAGCAATCGCTCAGCTCAAACTCCTCCCAATGCTGG 7970

QY 421 GATTACAGG-CGTGAGCCACCGGCGGCTGAGTAACTCTTAATCAGAGATTTTAAA 479

Db 7971 GATTACAGGCGGTGAGCCACCGGCGGCTGAGTAACTCTTAATCAGAGATTTTAAA 8030

QY 480 AGAACTTCTGCGCCACCACTTAACAATATCTCTCACTCACTCACTCACTCACTCACT 539

Db 8031 NNN 8090

QY 540 GCTAATAGTACCTAATTTTGTAGTAGGCTGCTGTTTATACATATATC 587

Db 8091 NNN 8138

RESULT 8
AL356309/c
LOCUS Human DNA sequence from clone Rp11-205K6 on chromosome 9, complete sequence.
DEFINITION
ACCESSION AL356309
VERSION AL356309.23 GI:1837596
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 44255)
Direct Submission
Submitted (18-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Jan 25, 2002 this sequence version replaced gi:16973835.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/projects/c_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9

Rp11-205K6 is from the library RPI1-11.1 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACE3.6
IMPORTANT: This sequence is not the entire insert of clone Rp11-205K6. It may be shorter because we sequence overlapping sections only once, except for a short overlap.
The true left end of clone Rp11-123K19 is at 42256 in this sequence. The true right end of clone Rp11-494N15 is at 2000 in this sequence.

FEATURES
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1.44255
/organism="Homo sapiens"
/db xref="taxon:9606"
/chromosome="9"
/clone="Rp11-205K6"
/clone_lib="RPI1-11.1"
BASE COUNT 11485 a 11569 c 10681 g 10520 t
ORIGIN

Query Match 17.8%; Score 203.4; DB 9; Length 44255;
Best Local Similarity 65.1%; Pred. No. 5.1e-46;
Matches 300; Conservative 0; Mismatches 161; Indels 0; Gaps 0;
QY 161 TTTTCTTTTGTGTTTCTCTGTCTGTCACCCAGCTGAGTACAGTGGTGTAGCTCAGG 220
Db 33974 TTTTCTTTGAGACAGGGTTTGTCTGTGTCGCCAGCTGGAGTGCAGTGGTGTATCATGA 33915
QY 221 CTCACTGAGCTTTGACCTCCAGCTCAAGTGTATCTCTGCTCAGCTTTCCTCAAGTAA 280
Db 33914 CTCACTGAGCTCAACCTCCGGGCTCAAGAGATCTCTCTACTCAGCTCCCAAGTAG 33855
QY 281 CTGGGACCAAGGATGATCACCACGCTAGGCTATTGTTTATACATTTTGTAGAGATG 340
Db 33854 CTGAGACCAAGGCTGACACCACTGTGTGCTAAATTTTAAAGTTTGTAGAGATA 33795
QY 341 GGGCTCTACCAATGTTGCCAGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGG 400
Db 33794 GGGCTCTCTATGTTGCCCAAGCTGGTCTGAACCTCTGGGCTCAAACTCTGCCACC 33735
QY 401 TCAACCTCCCAAAATGCTGGGATACAGGCTGAGCCACCGGCGGAGTAACTCC 460
Db 33734 TCAAGCTCCCAAGTGTGGGATACAGGCGGAGCACTGTGCTGCCCATTTAATAC 33675
QY 461 TAATCAGAGGATTTTAAAGAAACTTCTGCGCCACCCATTAACAATATCTCTACCA 520
Db 33674 TTTTAAATGCGCTTTTAAAGTGGGATTTCCCAATATATTTTCAAACTGCTGTATTAA 33615
QY 521 ATTTGGTAGTAATATTTGCTAAATAGTACCTAAATTTTAGGTAGGCACTGTGTTTATAC 580
Db 33614 AATATAGAAACTTACTTATTTCTGCTTTTCTTAATTTCTGTAGCCATTTTGCCAAACC 33555
QY 581 ATATATCCATTCCTCTTTTGTGTTGTTCTTTCTGTTTAAAT 621
Db 33554 CCTTTTGTAGTCTTAATAATTTCTAAATGATTATTGAT 33514

RESULT 9
AC079927/c
LOCUS Homo sapiens BAC clone Rp11-702A23 from 4, complete sequence.
DEFINITION
ACCESSION AC079927
VERSION AC079927.5 GI:18071472
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 84577)
REFERENCE
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792

```

PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
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REFERENCE
AUTHORS
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REFERENCE
AUTHORS
TITLE
JOURNAL

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

9847074
2 (bases 1 to 84577)
Cedroni,M., Abbott,A. and Boyer,E.
The sequence of Homo sapiens BAC clone RP11-702A23
Unpublished (2001)
3 (bases 1 to 84577)
Waterston,R.H.
Direct Submission
Submitted (17-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 84577)
Waterston,R.H.
Direct Submission
Submitted (05-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 84577)
Waterston,R.
Direct Submission
Submitted (21-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jan 5, 2002 this sequence version replaced gi:16924160.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.wustl.edu
----- Summary Statistics
Center project name: H_NH0702A23
-----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frenken,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.chori.org
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-757K22, 2000 bp overlap;
the clone sequenced to the right is RP11-19P13. Actual start of
this clone is at base position 110812 of RP11-757K22; actual end is
at base position 84577 of RP11-702A23.

Two transposons occurred in the growth of the clone that have been

```

```

FEATURES
source
omitted from the finished sequence.
Location/Qualifiers
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/db_xref="taxon:9606"
/chromosomes="4"
/map="4"
/clone="RP11-702A23"
/clone_lib="RPCI-11"
1..206
/repeat_region
/repeat_family="Alu"
256..528
/repeat_region
/repeat_family="Alu"
697..723
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/repeat_family="(TTTC)n"
713..846
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/repeat_family="Alu"
1407..1747
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/repeat_family="MER1_type"
1799..2262
/repeat_region
/repeat_family="L2"
2265..2290
/repeat_region
/repeat_family="(TTTTA)n"
2266..2574
/repeat_region
/repeat_family="Alu"
2599..2719
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2891..2996
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3255..3607
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/repeat_family="MER2_type"
3620..3713
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3637..3719
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4055..4083
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4056..4358
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4698..4721
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/repeat_family="MaLR"
6970..7010
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/repeat_family="(TTC)n"
6985..7294
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/repeat_family="Alu"
7703..7992
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8526..8559
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/repeat_family="(T)n"
8532..8840
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9438..9458
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9440..9738
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9744..9886
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10404..10507
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11088..11207
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11501..11662
/repeat_region
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11639..11846
/repeat_region
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11847..11971
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11972..12012
/repeat_region
/repeat_family="L2"

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repeat_region	12264..12438	/rpt_family="L1"	17.5%; Score 199.4; DB 9; Length 84577;	0;
repeat_region	12501..12536	/rpt_family="AT_rich"	Best Local Similarity 70.6%; Pred. No. 8.2e-45;	0;
repeat_region	12532..12646	/rpt_family="L2"	Matches 266; Conservative 0; Mismatches 111; Indels 0; Gaps 0;	0;
repeat_region	12653..12937	/rpt_family="Alu"		
repeat_region	12926..13023	/rpt_family="GA-rich"		
repeat_region	13003..13641	/rpt_family="L2"		
repeat_region	13678..13982	/rpt_family="Alu"		
repeat_region	13956..13982	/rpt_family="(A)n"		
repeat_region	14086..14470	/rpt_family="L1"		
repeat_region	14471..14773	/rpt_family="Alu"		
repeat_region	14775..15060	/rpt_family="Alu"		
repeat_region	15035..15081	/rpt_family="AT_rich"		
repeat_region	16498..16803	/rpt_family="Alu"		
repeat_region	16785..16806	/rpt_family="(TAAA)n"		
repeat_region	16931..17069	/rpt_family="MIR"		
repeat_region	17176..17466	/rpt_family="Alu"		
repeat_region	17329..17352	/rpt_family="AT_rich"		
repeat_region	17644..17768	/rpt_family="L1"		
repeat_region	17769..17969	/rpt_family="MIR"		
repeat_region	18032..18183	/rpt_family="L1"		
Query Match				
Best Local Similarity 70.6%; Pred. No. 8.2e-45;				
Matches 266; Conservative 0; Mismatches 111; Indels 0; Gaps 0;				
QY	161	TTTTTCTTTTGTCTTTCTCTGTCACCCAGGCTGAAGTACAGTGGTTAGTCAAGG	220	
Db	12935	TCTTTCTTTCAGGGGGTGTGCTCTGTCAACCCAGGCTGGAGTACAGTGGTATGATCAG	12876	
QY	221	CTCACTGAGCTTTGACCTCCAGGCTCAAGTATCTCTCTGCTCAGCTTTTCCAACTAA	280	
Db	12875	CTCACTGAGCTTTGACCTCTAGGCTCAAGTATCTCTCTTACCTCAGCCCTGAGTAG	12816	
QY	281	CTGGGACACAGGCTGATCATCACACGCTAGGCTATTGTTTACATTTTGTAGAGATG	340	
Db	12815	CTGGGGCCACAGTATACACACACACACACGCTAATTTTCTATTTTGTAGAGACA	12756	
QY	341	GGGTCTCACATGTTGGCCAGGTTGTTCTCAACTCTGGCTCAAGCAATCCGCTCAG	400	
Db	12755	GAGTCTCACTTTGTTGGCCAGGCTGTTCTCAAACTCTTGAGTCAAGCAATCTTCCGCC	12696	
QY	401	TCAACTCTCCCAATGCTGGGATTACAGGCTGAGCCACCGGCTGAGTAATTC	460	
Db	12695	TCAGCATCCCAAGTCTGGGATTACAGGTTGAGCCACACGCTGCTCATTTCT	12636	
QY	461	TAATCAGGATTTTAAAGAAATCTCTGGCCACCCATTAACAATATCTCTACCA	520	
Db	12635	CAATATTAGTTTCTCTCACTTCCATTTCAACAAACACCATCATGTCATATACCTTGATA	12576	
QY	521	ATTGGTAGTAATATT	537	
Db	12575	AATGAGAAATTTATTATT	12559	

RESULT 10	AC117414	143721 bp	DNA	linear	PRI 30-APR-2002
LOCUS	Homo sapiens 3 BAC RP11-48F14	(Roswell Park Cancer Institute Human BAC library) complete sequence.			
DEFINITION	AC117414				
ACCESSION	AC117414.3	GI:20340432			
VERSION					
KEYWORDS	HTG.				
SOURCE	Homo sapiens.				
ORGANISM	Homo sapiens				
REFERENCE	1 (bases 1 to 143721)				
AUTHORS	Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amarantunge, H.C., Are, J.R., Ayele, M., Banks, T., Barbara, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flaggs, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Hernandez, J., Harris, K., Hart, M., Havlak, P., Hawes, A., He, X., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Johnson, R., Jolivet, S., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., King, L., Korvah, J., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Lewis, L.C., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louisleg, H., Lozano, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapua, P., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Mei, G., Metzger, M., Miner, Z., Miner, Z., Mitchell, T., Monabhat, K., Moore, S., Morgan, M., Moorish, T., Morris, S., Moser, M., Nguyen, N., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Ogih, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Ruiz, S., Savary, G., Scher, S., Scott, G., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Sonaike, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamaria, A., Tamaria, K., Tang, H., Tansey, J., Taylor, C., Taylor, F., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalón, D., Vinson, R., Wang, Q., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S., Williams, G., Williamson, A., Wleczky, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Naylor, S.L., Weinstock, G. and Gibbs, R.				
TITLE	Direct Submission				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 143721)				
AUTHORS	Worley, K.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (10-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA				
REFERENCE	3 (bases 1 to 143721)				
AUTHORS	Worley, K.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (29-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA				
REFERENCE	4 (bases 1 to 143721)				
AUTHORS	Worley, K.C.				
TITLE	Direct Submission				
JOURNAL	Submitted (30-APR-2002) Human Genome Sequencing Center, Department				

357 CCAGGTTGGTCTCAAACTCTCGGCTCAAGCAATCCGCTCAAGCTCAACCTCCCAATG 416
 121244 CCAGGTTGGTCTCGAACTCTCTGGCTCAAGCAATCCGCTCAAGCTCAACCTCCCAATG 121185
 417 CTGGGATTACAGCGGTGAGCCACCGGCGCCAGGCTGAGTAATCTTAATCAGAGTTTGA 476
 121184 CTGAGATTACAGCGGTGAGCTACTGTCTGGCCAAAGTATGTGTTTATCCCACTTT 121125
 477 AAAGAAATCTCTGCGCCACCCATTAAACA 507
 121124 TAAGTGAAGAATCTGAGCCTCAAAATCACAGA 121094

RESULT 11
 LOCUS AK023951/c 2343 bp mRNA linear PRI 01-AUG-2002
 DEFINITION Homo sapiens cDNA FLJ13889 fis, clone THYR01001595.
 ACCESSION AK023951
 VERSION AK023951.1 GI:10436049
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Homo sapiens thyroid gland cDNA to mRNA, clone lib:THYR01 clone:THYR01001595.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 AUTHORS Isogai, T., Ota, T., Hayashi, K., Sugiyama, T., Otsuki, T., Suzuki, Y., Nishikawa, T., Nagai, K., Sugano, S., Ishibashi, T., Fujimori, K., Tanai, H., Kimata, M., Watanabe, M., Hirakawa, S., Ishii, S., Kawai, Y., Saito, K., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagahara, K., Masuho, Y. and Kanehori, K.
 TITLE NEDO human cDNA sequencing project
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2343)
 AUTHORS Isogai, T. and Otsuki, T.
 TITLE Direct Submission
 JOURNAL Submitted (23-AUG-2000) Takao Isogai, Helix Research Institute, Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 252-0812, Japan (E-mail: genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
 COMMENT NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing. Research Association for Biotechnology; cDNA library construction, 5'- and 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology; Institute of Medical Science, University of Tokyo.

FEATURES
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 /db_xref="taxon:9606"
 /clone="THYR01001595"
 /tissue_type="thyroid gland"
 /clone_lib="THYR01"
 /note="cloning vector: pME18SFL3"
 BASE COUNT 603 a 515 c 535 g 690 t
 ORIGIN

Query Match 17.1%; Score 195; DB 9; Length 2343;
 Best Local Similarity 80.6%; Pred. No. 5.7e-44;
 Matches 228; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
 177 TTTTGTCTGTACCCAGGCTGAAGTACAGTGGTGTAGCTCAGGCTCACTGAGCTTTGA 236
 2331 TCTGTGTCTGTACCCAGGCTGAAGTACAGTGGTGTAGCTCAGGCTTTGA 2272
 237 CTCTCCAGGCTCAAGTATCTCTCTCTCAGCTTTCCAGTAACTGGACACAGGAT 296
 2271 CTCTCCAGGCTCAGGTGATCTCTCCACCTCAGGCTCCGAGTAGTGGACTACAGGAT 2212
 297 GCATCACCAGCTAGGCTATTGTTTACATTTTGTAGAGATGGGCTCTCACCAGTTG 356
 2211 GCACCAACCGTCCAGCTAAATTTTGTACTTTTGTAGAGACGGGTTTACCAGTTG 2152

357 CCAGGTTGGTCTCAAACTCTCGGCTCAAGCAATCCGCTCAAGCTCAACCTCCCAATG 416
 2151 CACAGGTTGGTCTCAAGCTCTCTGGCTCAAGCTCAAGCTCAACCTCCCAATG 2092
 417 CTGGGATTACAGCGGTGAGCCACCGGCGCCAGGCTGAGTAATC 459
 2091 CTGGGATTACAGCGGTGAGCCACCGGCTGAGCTGAGTATC 2049

RESULT 12
 LOCUS AL133390 71872 bp DNA linear PRI 04-JAN-2001
 DEFINITION Human DNA sequence from clone RPI-317G22 on chromosome 1 Contains part of the KMO (kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)) gene, the CHML(choroideremia-like (Rab escort protein 2)) gene, the gene for encephalopain, ESTs, STSs, GSSs and a CpG Island, complete sequence.
 ACCESSION AL133390
 VERSION AL133390.7 GI:7406530
 KEYWORDS HTG.
 SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 71872)
 AUTHORS Parker, A.
 TITLE Direct Submission
 JOURNAL Submitted (04-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 COMMENT On Apr 3, 2000 this sequence version replaced gi:7320611. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence is the entire insert of clone RPI-317G22 This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chri RPI-317G22 is from the library RPI-1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
 VECTOR: pCIPAC2. Location/Qualifiers
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 /db_xref="taxon:9606"
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 /clone="RPI-317G22"
 /clone_lib="RPI-1"
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 /note="LIPBb repeat: matches 30..2559 of consensus"
 repeat_region
 2509..2919
 /note="LIPBa repeat: matches 601..1014 of consensus"
 repeat_region
 2920..3281
 /note="THL1B repeat: matches 1..364 of consensus"
 repeat_region
 3282..4433
 /note="LIPBa repeat: matches -1481..601 of consensus"
 repeat_region
 4539..7775


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8425. .8631
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/notes="match: GSS: Em:AQ882365"
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10800. .10849
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16127. .19815)
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(kynurenine 3-hydroxylase))"
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/db_xref="GI:12043384"
/tranlations="GFEDCLVDELMDKESNDLSCLPVPFSLRIPDDHAISDLSNYY
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INKGLFGLSLAISYLLIHYMSRSLRRPWNIAHFRNTTCPPAKAVDSLEQ
ISNLSIR"
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repeat_region /notes="AluX repeat: matches 2. .292 of consensus"
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repeat_region 12485. .12534
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/notes="match: STS: Em:G09117"

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Query Match 17.1%; Score 195; DB 9; Length 71872;
Best Local Similarity 65.2%; Pred.No. 1.4e-43;
Matches 302; Conservative 0; Mismatches 160; Indels 1; Gaps 1;
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||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: <http://www-seq.wi.mit.edu>
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L1869
 Center clone name: 115_G_24
 ----- Summary Statistics
 Sequencing vector: M13; M7815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 141535 bases at least Q40
 Consensus quality: 144279 bases at least Q30
 Consensus quality: 145529 bases at least Q20
 Insert size: 145000; agarose-fp
 Insert size: 146459; sum-of-contigs
 Quality coverage: 5.3 in Q20 bases; agarose-fp
 Quality coverage: 5.2 in Q20 bases; sum-of-contigs

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 9 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 2950: contig of 2950 bp in length
 * 2951 3050: gap of 100 bp
 * 3051 6314: contig of 3264 bp in length
 * 6315 6414: gap of 100 bp
 * 6415 11824: contig of 5410 bp in length
 * 11825 11924: gap of 100 bp
 * 11925 20145: contig of 8221 bp in length
 * 20146 20245: gap of 100 bp
 * 20246 30884: contig of 10639 bp in length
 * 30885 30984: gap of 100 bp
 * 30985 44984: contig of 14000 bp in length
 * 44985 45084: gap of 100 bp
 * 45085 77877: contig of 32793 bp in length
 * 77878 77977: gap of 100 bp
 * 77978 112578: contig of 34601 bp in length
 * 112579 112678: gap of 100 bp
 * 112679 147259: contig of 34581 bp in length.

 Location/Qualifiers
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 6415. 11824
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 221 CTCACGTGAGCTTTGACCTCCAGGCTCAAGTATCTCTGCTCAGCTTCCAGATAA 280
 10444 CTCACGTGACCTCCATCTCCAGGTTCAAGTGGTCTCTACCTCAGCTCCGAGTAG 10503
 281 CTGGGACACAGGCTATCAGGCTATCAGGCTATGTTTACATTTTTTGTAGATG 340
 10504 CTGGGACACAGGCTATCAGGCTATCAGGCTATGTTTACATTTTTTGTAGATG 10563
 341 GGGTCTCACATTTGCCAGGTTGCTCAAACTCTGGCTCAAGCAATCCGCTCAGC 400
 10564 GGGTCTCATCTTTGCCAGGCTGATCTCAAACTCTGGCTCAAGCAATCCGCTCAGC 10623
 401 TCAACTCCCAATCTGGATTTACAGGCTGAGCCAGGCTGAGGCTGAGTAATCC 460
 10624 TCGGCTCCCAATCTGGATTTACAGGCTGAGGCTGAGGCTGAGGCTGAGTCA 10683
 461 TAATCAGGATTTTAAAGAACTTCTGCGCCACCCATTAACAATATCTCTACCA 520
 10684 TTTTACCATTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 10743
 521 ATTGGTGAATTAATATTTTGGTAAATAGTACCTAAATTTTGGTGGCTGCTGTTATA 579
 10744 ACAGTGTATGAATATCTTCCCAATGAATATCTTCAAAATCAATGAATGAATGTTT 10803
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RESULT 13
 AC019248 147259 bp DNA linear HTG 28-FEB-2000
 LOCUS Homo sapiens clone RP11-115G24, WORKING DRAFT SEQUENCE, 9 unordered
 DEFINITION
 AC019248.3 GI:7107772
 VERSION HTGS PHASE1; HTGS_DRAFT.
 KEYWORDS
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 147259)
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 Homo sapiens chromosome, clone RP11-115G24
 Unpublished
 2 (bases 1 to 147259)
 Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Bida, F.,
 Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Castle, A.,
 Chospel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
 DeArrellano, K., Dewar, K., Domino, M., Doyle, M., Fenster, J.,
 Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J.,
 Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
 Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
 Landers, J., Lehoczy, J., Levine, R., Liu, C., Liu, G., Locke, K.,
 MacDonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K.,
 McPheeters, R., Meldrum, J., Meneus, I., Morrow, J., Naylor, J.,
 Norman, C.H., O'Connor, T., O'Donnell, P., Oliver, T.M., Peterson, K.,
 Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D.,
 Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
 Stojanovic, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
 Tirrell, A., Vasiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J.,
 Zimmer, A. and Zody, M.

Direct Submission
 Submitted (31-DEC-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Feb 28, 2000 this sequence version replaced gi:6730909.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
<http://fcp.genome.washington.edu/RM/RepeatMasker.html>
 ----- Genome Center

ORIGIN

Query Match 17.1%; Score 195; DB 2; Length 147259;
 Best Local Similarity 80.6%; Pred. No. 1.7e-43;
 Matches 228; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

QY 177 TTTTGTCTCTACCCAGGCTGAAGTACAGTGTAGTCTCAGGCTCAGTGCAGCTTTGA 236
 |||||
 Db 141121 TCTTGTCTCTACCCAGGAGTGCAGTGCAGGATCACTGCTCACTGCAGCTTTGA 141180
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 QY 237 CTTCCAGGCTCAAGTATCTCTGCTCTCAGCTTTCCAGTAACTGGGACACACGCGCAT 296
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 Db 141181 CTTCCAGGCTCAGGTATCTCTCCACCTCAGCTCCGAGTACGCTGAGCTACAGCAT 141240
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 QY 297 GCATCACCCAGCTAGGCTATTTGTTTACATTTTGTAGAGATGGGTCTCACCATTGTTG 356
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 Db 141241 GCACCAACCACTGCTCAATTTTGTACTTTTGTAGAGACGGGTTTCAACATGTTG 141300
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 Db 141301 CACAGCTGGTCTCAGACTCTCTGGGCTCAAGCTATCGGCTGCTCGGCTCCCAAATG 141360
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 Db 141361 CTGGATTACACTGGAGCCACCGTGCCTCGGCGCCGAGATCTC 141403
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RESULT 14

AL365215

LOCUS

AL365215 Human DNA sequence from clone RP11-41608 on chromosome 10, complete
 sequence.

ACCESSION

AL365215

VERSION

AL365215.23

KEYWORDS

HTG.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

Ashwell, R.

TITLE

Direct Submission

JOURNAL

Submitted (23-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonesrequest@sanger.ac.uk

COMMENT

On Jun 22, 2001 this sequence version replaced gi:14456224.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 This sequence was finished as follows unless otherwise noted: all
 regions were either double-stranded or sequenced with an alternate
 chemistry or covered by high quality data (i.e., phred quality >= 30);
 an attempt was made to resolve all sequencing problems, such
 as compressions and repeats; all regions were covered by at least
 one plasmid subclone or more than one M13 subclone; and the
 assembly was confirmed by restriction digest. The following
 abbreviations are used to associate primary accession numbers given
 in the feature table with their source databases: Em.; EMBL; SW.;
 SWISSPROT; Tr.; TREMBL; Wp.; WORMPEP; Information on the WORMPEP
 database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
 This sequence was generated from part of bacterial clone contigs of human
 chromosome 10, constructed by the Sanger Centre Chromosome 10
 Mapping Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr10>
 RP11-41608 is from the library RP11-11.2 constructed by the group
 of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
 VECTOR: pBACE3.6
 This sequence is the entire insert of clone RP11-41608 The true

FEATURES

source

left end of clone RP11-320B8 is at 101956 in this sequence.

Location/Qualifiers

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 19355. .19657
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 20104. .20153
 /note="L2 repeat: matches 2627. .2676 of consensus"
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 46510. .46702
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 DB 19444 CTTCCAGGCTCAGTGATCTCTCCACCTCAGCTCCGAGTAGCTGGACTACAGCAT 19503
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 DB 19504 GCACCACACGCTCCAGCTAAATTTTGTACTTTTGTAGAGACGGGTTTCCCATGTTG 19563
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 AC090104.4 GI:22123547
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 SOURCE human.
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 Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 Birren,B., Nusbaum,C. and Lander,E.
 1 (bases 1 to 164167)
 Homo sapiens chromosome 8, clone RP11-451E11
 Unpublished
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
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 AUTHORS
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
 Baran,N., Bastien,V., Boguslavskiy,L., Boukhgalter,B., Brown,A.,
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 Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 19:00:12 ; Search time 302 Seconds
(without alignments)
8508.378 Million cell updates/sec

Title: US-09-617-174C-1

Perfect score: 1141

Sequence: 1 agataagcacagcagagaag.....aggataactgtgactccagg 1141

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1137.8	99.7	1141	18	Human maspin promo
2	745.4	65.3	12426	22	Tumour suppressor
3	723.4	63.4	12426	22	Tumour suppressor
4	195	17.1	568	22	Human cDNA clone (
5	195	17.1	2343	22	Human cDNA sequenc
6	190.2	16.7	66804	24	Human transporter
7	185.4	16.2	916	22	Human reproductive
8	185.4	16.2	32184	22	Human nervous syst
9	185.4	16.2	32184	22	Human nervous syst

10	185.4	16.2	38272	22	AAK84952	Human immune/haema
11	185.4	16.2	38348	22	AAK84953	Human immune/haema
12	184.6	16.2	240825	22	AAF24497	Human PG-3 gene.
13	184	16.1	1162	21	AAC79682	Human secreted pro
14	183.4	16.1	735	22	AAK05557	Human reproductive
15	183.4	16.1	735	22	AAK89703	Human digestive sy
16	182.6	16.0	227968	24	ABK83497	Human cDNA differe
17	182.6	16.0	1956	22	ABA21277	Human nervous syst
18	182.2	16.0	14748	24	ABK51275	Human Caspase-2, C
19	182.2	16.0	17026	22	AAK70372	Human immune/haema
20	181.4	15.9	17424	24	ABK68122	Ovary cancer relat
21	181.2	15.9	1519	20	AAZ10674	cDNA encoding a hu
22	181.2	15.9	103747	24	ABQ88139	Human osteoblast d
23	180.8	15.8	1421	22	AAK73297	Human immune/haema
24	180.4	15.8	21477	22	AAK66626	Human immune/haema
25	180.4	15.8	21480	22	AAK66625	Human immune/haema
26	180	15.8	21470	23	ABK42270	Genomic sequence #
27	179.8	15.8	1423	22	AAF27785	Human MANGO 347 co
28	179.8	15.8	1440	21	AAC90029	Clone HTHCW70 codi
29	179.8	15.8	1442	22	AAH33267	Human colon cancer
30	179.4	15.7	1248	24	AAD33244	Human secreted pro
31	179.2	15.7	5269	22	AAK80329	Human immune/haema
32	179	15.7	7233	22	AAK36623	Human cardiovascular
33	178.8	15.7	8053	22	AAI98931	Human excretory re
34	178.8	15.7	8053	22	AAI63281	Human kidney relat
35	178.8	15.7	10241	22	AAK83768	Human immune/haema
36	178.8	15.7	10241	22	AAK33394	DNA encoding human
37	178.6	15.7	1125	22	ABA06543	Human cDNA SQ ID
38	178.6	15.7	1125	22	AAK28831	Human immunoglobul
39	178.6	15.7	66804	24	ABK87050	Human transporter
40	178.4	15.6	16181	22	AAK04268	Human reproductive
41	178.4	15.6	16181	23	ABK42539	Genomic sequence #
42	178	15.6	5962	23	AAK82348	DNA encoding novel
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44	177.8	15.6	700	20	AAK30339	DNA encoding a hum
45	177.8	15.6	175737	24	ABK83571	Human cDNA differe

ALIGNMENTS

RESULT 1	AAK89000	standard; cDNA; 1141 BP.
ID	AAK89000	standard; cDNA; 1141 BP.
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XX	AAK89000;	
DT	22-APR-1998	(first entry)
DE	Human maspin promoter and partial coding cDNA.	
DE	Human maspin promoter and partial coding cDNA.	
KW	Human maspin promoter and partial coding cDNA.	
KW	Human maspin promoter and partial coding cDNA.	
OS	Homo sapiens.	
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XX DE Human cDNA clone (3'-primer) SEQ ID NO:10310.
 XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX OS Homo sapiens.
 XX PN EP1074617-A2.
 XX PD 07-FEB-2001.
 XX PP 28-JUL-2000; 2000EP-0116126.
 XX PR 29-JUL-1999; 99JP-0248036.
 XX PR 27-AUG-1999; 99JP-0300253.
 XX PR 11-JAN-2000; 2000JP-0118776.
 XX PR 02-MAY-2000; 2000JP-0183767.
 XX PR 09-JUN-2000; 2000JP-0241899.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
 XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX DR WPI; 2001-318749/34.
 XX PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX PS Claim 3; SEQ ID 10310; 2537pp + CD ROM; English.
 XX CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
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 Query Match 17.1%; Score 195; DB 22; Length 568;
 Best Local Similarity 80.6%; Pred. No. 2.9e-43;
 Matches 228; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
 QY 177 TTTTGTCTGTCTACCCAGGCTGAAGTACAGTGTAGCTCAGCGCTCAGTGCAGCTTTGA 236
 DB 13 TCTTGTCTGTCTACCCAGGCTGAAGTACAGTGTAGCTCAGCGCTCAGTGCAGCTTTGA 72
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 QY 297 GCATACACCGCTAGGCTATTGTTTACATTTTGTAGAGATGGGCTCACCATTGTG 356
 DB 133 GCACCAACCGCTCCAGCTAAATTTTGTACTTTTGTAGAGACGGGTTTACCATTGTTG 192

QY 357 CCAGGTTGGTCTCAAACTCTCGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAATG 416
 DB 193 CACAGGCTGGTCTCAGACTCTCGGCTCAAGCTATCCGCTTGGCTCCCAAGTG 252
 QY 417 CTGGGATTACAGGCTGAGCCACCGGGCCAGGCTGAGTAATC 459
 DB 253 CTGGGATTACAACTGGGAGCCACCGTGCCTCCGCGCCGAGATCTC 295
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 XX DT 26-JUN-2001 (first entry)
 XX DE Human cDNA sequence SEQ ID NO:15908.
 XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
 XX OS Homo sapiens.
 XX PN EP1074617-A2.
 XX PD 07-FEB-2001.
 XX PP 28-JUL-2000; 2000EP-0116126.
 XX PR 29-JUL-1999; 99JP-0248036.
 XX PR 27-AUG-1999; 99JP-0300253.
 XX PR 11-JAN-2000; 2000JP-0118776.
 XX PR 02-MAY-2000; 2000JP-0183767.
 XX PR 09-JUN-2000; 2000JP-0241899.
 XX PA (HELI-) HELIX RES INST.
 XX PI Ota T, Isogai T, Nishikawa T, Hayaashi K, Saito K, Yamamoto J;
 XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX DR WPI; 2001-318749/34.
 XX PT Primer sets for synthesizing polynucleotides, particularly the 5602
 PT full-length cDNAs defined in the specification, and for the detection
 PT and/or diagnosis of the abnormality of the proteins encoded by the
 PT full-length cDNAs -
 XX PS Claim 8; SEQ ID 15908; 2537pp + CD ROM; English.
 XX CC The present invention describes primer sets for synthesizing 5602
 CC full-length cDNAs defined in the specification. Where a primer set
 CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
 CC to the complementary strand of a polynucleotide which comprises one of
 CC the 5602 nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in
 CC the specification. The primer sets can be used in antisense therapy and
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
 CC represent oligonucleotides, all of which are used in the exemplification
 CC of the present invention.
 XX CC

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AC	ABK87050;
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DT	07-OCT-2002 (first entry)
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KW	Human; gene; ds; transporter protein; htp; chromosome 12;
KW	Na-dependent inorganic phosphate co-transporter; cell proliferation;
KW	cell differentiation; cell signalling; gene therapy; protein therapy;
KW	antigen; vaccine; diagnosis; single nucleotide polymorphism; SNP.
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OS	Homo sapiens.
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PR	20-OCT-2000;	2000US-0241808.
PR	20-OCT-2000;	2000US-0241809.
PR	20-OCT-2000;	2000US-0241826.
PR	01-NOV-2000;	2000US-0244617.
PR	08-NOV-2000;	2000US-0246474.
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PR	08-NOV-2000;	2000US-0246532.
PR	08-NOV-2000;	2000US-0246538.
PR	08-NOV-2000;	2000US-0246609.
PR	08-NOV-2000;	2000US-0246610.
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PR	08-NOV-2000;	2000US-0246613.
PR	17-NOV-2000;	2000US-0249207.
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PR	17-NOV-2000;	2000US-0249215.
PR	17-NOV-2000;	2000US-0249216.
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PR	08-DEC-2000;	2000US-0251980.
PR	08-DEC-2000;	2000US-0251989.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.

Rosen CA. Barash SC, Ruben SM;

Isolated nucleic acid molecule encoding a reproductive system antigen is used in preventing, treating or ameliorating a medical condition -

Disclosure: SEQ ID NO 8218: 1297pp + Sequence Listing; English.

The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention.

XX

```
SQ Sequence 916 BP; 255 A; 192 C; 239 G; 230 T; 0 other;
Query Match 16.2%; Score 185.4; DB 22; Length 916;
Best Local Similarity 75.2%; Pred. No. 1.5e-40;
Matches 231; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
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DB 911 TCTCACTCTGTACCCAGGCTGGAGTGCAGTGCATGATCCCGGCTCACGGCAACCTGTG 852
QY 237 CTTCCAGGCTCAAGTATCTCTCTCTCAGCTTTCCAGTAACTGGGACACACAGCAT 296
DB 851 CTTCTGGGTTCAAGTATCTCTCTCAGCTCCCAAGTAGCTGGGACACAGTGC 792
QY 297 GCATCACCGCTAGGCTATTTGTTTACATTTTGTAGAGATGGGTCTCCACCATGTTG 356
DB 791 ACATCACACACCTGGCTAATCTTTGTTATTTTGTAGAGATGGGTTCACCATGTTG 732
QY 357 CCAGGTTGGTCTCAAACTCTGGGCTCAAGCAATCGGCTCAGTCACCTCCCAAAATG 416
DB 731 GCCAGGTTGGTCTCAAACTCTGACCTCAAGTATCGGCCACCTCGGGCTCCCAAGTG 672
QY 417 CTGGATTACAGCGCTGAGCCACCGGSCCAGGCTGAGTAATCCTAATCACAGGATTTTA 476
DB 671 CTGGATTATAGCGCGAGCCACCGCGCGGCTTTTATTGTTAATTTAAAAATTA 612
QY 477 AAAAGAA 483
DB 611 AATAAA 605

RESULT 8
ID ABA20589
ID ABA20589 standard; DNA; 32184 BP.
XX AC ABA20589;
XX DT 23-JAN-2002 (first entry)
XX DE Human nervous system related polynucleotide SEQ ID NO 12920.
XX KW Human; nootropic; neuroprotective; cytostatic; dermatological; virucide;
XX KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary;
XX KW antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer;
XX KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
XX KW antiallergic; antidiabetic; antitumor; anticonvulsant; antifungal;
XX KW antiparasitic; cardiant; immune disorder; cardiovascular disorder;
XX KW neurological disease; infection; nephrotropic; gene therapy; vaccine; ds.
OS Homo sapiens.
XX PN WO200159063-A2.
XX PD 16-AUG-2001.
XX PF 17-JAN-2001; 2001WO-US01334.
XX PR 31-JAN-2000; 2000US-0179065.
XX PR 04-FEB-2000; 2000US-0180628.
XX PR 24-FEB-2000; 2000US-0184664.
XX PR 02-MAR-2000; 2000US-0186350.
XX PR 16-MAR-2000; 2000US-0189874.
XX PR 17-MAR-2000; 2000US-0190076.
XX PR 18-APR-2000; 2000US-0198123.
XX PR 19-MAY-2000; 2000US-0205515.
XX PR 07-JUN-2000; 2000US-0209467.
XX PR 28-JUN-2000; 2000US-0214886.
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PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0244674.
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CC epilepsy; and (f) infectious diseases such as viral, bacterial, fungal
CC and parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from wipo.int/pub/published pct sequences.

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				Gaps 0

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2304 TGGAGTGCAGTGGGTATGATCTTTGGGCTCACTTCAGGCTTGAACCTCCAGGGCTCAAGAGGTC 2386
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257 CTCTCGCTCTCAGCTTTCCAAAGTAACTGGGACCAAGGCAATGCATCAACCCTAGGCTAT 316
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Db 2364 CTCCTGCTTCAGCCCCCCCAGTAGCTGGACTACAGGAGTGGCGCCACCTCTAGTAA 2423

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QY 377 CTGGGCTCAAGCAATCCGCTCAGTCACCTCCCAAAATGCTGGGATTACAGGCGTGAAC 436

QY	437	CACCGGCCAGGGCT	451

Db 2544 CACTACCCCTGGCCT 2558

RESULT 9
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Human; nontropic; neuroprotective; cytostatic; dermatological; virucide;
immunosuppressive; anti-inflammatory; anti-HIV; antibacterial; vulnery;
antipneumonic; antiparasitic; antitubercular; antiparasitic; cancer;

[illegible]

neurological disease; infection; nephrotropic; gene therapy; vaccine; us

XX WO200159063-A2. XX
XX PN XX

PD	16-AUG-2001.
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PF	17-JAN-2001; 2001WO-US01334.

31-JAN-2000; 2000US-0179065.
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PR 01-DEC-2000; 2000US-0250391.
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PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.

PR	08-DEC-2000; 2000US-0251856.
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PR	08-DEC-2000; 2000US-0251868.

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PR	08-DEC-2000;	2000US-0251990.
PR	08-DEC-2000;	2000US-0251997.

PR 05-JAN-2001; 2001US-0259678.
XX.
XX. (HUMAN-1) HUMAN GENOME SCI INC.
DA DA

XX
PI
XX
Rosen CA, Barash SC, Ruben SM;
XX

XX Nucleic acids encoding 3224 human nervous system antigen polypeptides,
DR WPI; 2001-541565/60.

PT useful for preventing, diagnosing and/or treating
cancers and metastases -
XX

The invention relates to novel genes (ABA11004-ABA21534) and proteins

CC medical conditions e.g. by protein or gene therapy. The genes are
CC isolated from a range of human tissues disclosed in the specification.
CC The nucleic acids, proteins, antibodies and (ant)agonists are useful
CC

CC in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (c) and (d) cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital;

CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC disease, multiple sclerosis, rheumatoid arthritis and ulcerative
CC haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's
CC immune disorders e.g. Addison's disease, diabetes mellitus, Crohn's
CC immune disorders e.g. Addison's disease, diabetes mellitus, Crohn's

CC (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and

PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
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PR 05-JAN-2001; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-541565/60.

Nucleic acids encoding 3224 human nervous system antigen polypeptides, useful for preventing, diagnosing and/or treating nervous system cancers and metastases -

Disclosure; SEQ ID NO 12921; 1701pp + Sequence Listing; English.

The invention relates to novel genes (ABA11004-ABA21534) and proteins (ABP14678-ABP18001) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other cancers of the adrenal gland, bone, bone

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PR	08-NOV-2000;	2000US-0246610.
PR	08-NOV-2000;	2000US-0246611.
PR	17-NOV-2000;	2000US-0246613.
PR	17-NOV-2000;	2000US-0249207.
PR	17-NOV-2000;	2000US-0249208.
PR	17-NOV-2000;	2000US-0249209.
PR	17-NOV-2000;	2000US-0249210.
PR	17-NOV-2000;	2000US-0249211.
PR	17-NOV-2000;	2000US-0249212.
PR	17-NOV-2000;	2000US-0249213.
PR	17-NOV-2000;	2000US-0249314.
PR	17-NOV-2000;	2000US-0249315.
PR	17-NOV-2000;	2000US-0249316.
PR	17-NOV-2000;	2000US-0249317.
PR	17-NOV-2000;	2000US-0249318.
PR	17-NOV-2000;	2000US-0249324.
PR	17-NOV-2000;	2000US-0249345.
PR	17-NOV-2000;	2000US-0249354.
PR	17-NOV-2000;	2000US-0249265.
PR	17-NOV-2000;	2000US-0249297.
PR	17-NOV-2000;	2000US-0249299.
PR	01-DEC-2000;	2000US-0249300.
PR	01-DEC-2000;	2000US-0250160.
PR	01-DEC-2000;	2000US-0250391.
PR	05-DEC-2000;	2000US-0251030.
PR	05-DEC-2000;	2000US-0251988.
PR	05-DEC-2000;	2000US-0256719.
PR	06-DEC-2000;	2000US-0251479.
PR	08-DEC-2000;	2000US-0251856.
PR	08-DEC-2000;	2000US-0251869.
PR	08-DEC-2000;	2000US-0251989.
PR	08-DEC-2000;	2000US-0251990.
PR	11-DEC-2000;	2000US-0254097.
PR	05-JAN-2001;	2001US-0259678.
XX	(HUMA-)	HUMAN GENOME SCI INC.
XX	Rosen CA,	Barash SC, Ruben
PI	WPI:	2001-483426/52.
XX		
XX		
DR		

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis -

Disclosure; SEQ ID NO 39765; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased

		05-OCT-2000.
XX	PD	
XX	PF	22-MAR-2000; 2000WO-US07440.
XX	PP	
XX	PR	26-MAR-1999; 99US-0126503.
XX	RR	17-DEC-1999; 99US-0172409.
XX	PA	(HUMA-) HUMAN GENOME SCI INC.
XX	PI	Rosen CA, Ruben SM, Komatsoulis G;
XX	DR	WPT; 2000-594637/56.
XX	DD	P-PSTD; AAB44597.
XX	DT	Fifty nucleic acid molecules encoding human secreted proteins, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -
XX	PS	Claim 1; Page 338; 410pp; English.
XX	CC	The polynucleotide sequences given in AAC79681 to AAC79730 encode the human secreted proteins given in AAB44596 to AAB44645. AAB44646 to AAB44693 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; anti-allergic; hepatotrophic; antidiabetic; anti-inflammatory; anti-ulcer; vulnerable; anticoagulant; antibacterial; antifungal; antiparasitic; and cardiant. The polynucleotides and polypeptides are useful for preventing, treating or ameliorating a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The polynucleotides are useful for chromosome identification. They are also useful as probes for diagnosing a disorder related to the female reproductive system, particularly breast cancer and/or ovarian cancer. They are also useful in the gene therapy of breast cancer and ovarian cancer. The nucleic acids, protein, antibodies, agonists and antagonists from the present invention are useful in the diagnosis, treatment and prevention of: cancer; immune disorders; cardiovascular disorders; wound healing; neurological diseases; and infectious diseases. AAC79672 to AAC79680 and AAB44595 represent sequences used in the exemplification of the present invention.
XX	SQ	Sequence 1162 BP; 336 A; 218 C; 300 G; 308 T; 0 other;
	Query Match	16.1%; Score 184; DB 21; Length 1162;
	Best Local Similarity	75.3%; Pred. No. 4.le-40;
	Matches 229; Conservative	0; Mismatches 75; Indels 0; Gaps 0;
Qy	161	TTTTTTTCTTTTGTTTCCTGTCGCCAGCGGTGAAGTAGATCCTCTCGTCTCAGCTTTCCAAGTAA 1094
Dd	1153	TTTTTTTTTTTGGTCAAGATCTCTGTCACCTAGTGTGGAGTCAGTGGTGCCTCATATAA 1094
Qy	221	CTCACTGCAGCTTTGACTCTCCCAGGCTCAAAGTGATCCTCTCGTCTCAGCTTTCCAAGTAA 280
Dd	1093	TTCATTGCAGGCTCAACTCCCCAGCTCAAGTGATCTCTCCACCTCAACCTCCCGCAGCAG 1034
Qy	281	CTGGGACAACAGGCGATGCATCACACCCTAGGCTATTGTTTACATTTTTTGTAGAGATG 340
Dd	1033	CTGGGACTACAAGTGCCCTCCACCACGCTTGTTTAATTTTTTTGTATTTTTTTGTAGATG 974
Qy	341	GGGTCTCACCANTGTGCCAGGTGGTCTCAAACCTCTGGGCTCAAGAATCCGCTCAGC 400
Dd	973	GGGFTTTTACCANVTGTCACAGGCTGGTCTCGAACCTCTCGGCTCAAGTGATCTCTCCACC 914
Qy	401	TCAACCTCCCCAAAATGCTGGGATTTACAGGCGTGAGCCACCGGGCCAGSGGCTGAGTAATCC 460
Dd	913	TCTGTCTCCCNAAAGTGTGGGNTTTACAGGCATGAGCCACGACCGGGGGCAAAATTTTCCT 854
Qy	461	TAAT 464

PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232197.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0232403.
PR 14-SEP-2000; 2000US-0232406.
PR 14-SEP-2000; 2000US-0232407.
PR 14-SEP-2000; 2000US-0232408.
PR 14-SEP-2000; 2000US-0232409.
PR 14-SEP-2000; 2000US-0232410.
PR 14-SEP-2000; 2000US-0232411.
PR 14-SEP-2000; 2000US-0232412.
PR 14-SEP-2000; 2000US-0232413.
PR 14-SEP-2000; 2000US-0232414.
PR 14-SEP-2000; 2000US-0232415.
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PR 14-SEP-2000; 2000US-0232417.
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PR 14-SEP-2000; 2000US-0232421.
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PR 14-SEP-2000; 2000US-0232424.
PR 14-SEP-2000; 2000US-0232425.
PR 14-SEP-2000; 2000US-0232426.
PR 14-SEP-2000; 2000US-0232427.
PR 14-SEP-2000; 2000US-0232428.
PR 14-SEP-2000; 2000US-0232429.
PR 14-SEP-2000; 2000US-0232430.
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PR 14-SEP-2000; 2000US-0232450.
PR 14-SEP-2000; 2000US-0232451.
PR 14-SEP-2000; 2000US-0232452.
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PR 14-SEP-2000; 2000US-0232454.
PR 14-SEP-2000; 2000US-0232455.
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PR 14-SEP-2000; 2000US-0232459.
PR 14-SEP-2000; 2000US-0232460.
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PR 14-SEP-2000; 2000US-0232465.
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PR 14-SEP-2000; 2000US-0232467.
PR 14-SEP-2000; 2000US-0232468.
PR 14-SEP-2000; 2000US-0232469.
PR 14-SEP-2000; 2000US-0232470.
PR 14-SEP-2000; 2000US-0232471.
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PR 14-SEP-2000; 2000US-0232480.
PR 14-SEP-2000; 2000US-0232481.
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PR 14-SEP-2000; 2000US-0232490.
PR 14-SEP-2000; 2000US-0232491.
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PR 14-SEP-2000; 2000US-0232495.
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PR 14-SEP-2000; 2000US-0232498.
PR 14-SEP-2000; 2000US-0232499.
PR 14-SEP-2000; 2000US-0232500.

PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 06-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251899.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465570/50.
XX
XX Isolated nucleic acid molecule encoding a reproductive system antigen
XX is used in preventing, treating or ameliorating a medical condition -
XX
XX Disclosure; SEQ ID NO 8245; 1297pp + Sequence Listing; English.
XX
XX The present invention provides the protein and coding sequences of a
XX number of human reproductive system related antigens. These can be used
XX in the prevention and treatment of reproductive system disorders,
XX including cancer. The present sequence is a genomic sequence encoding a
XX protein of the invention.
XX
XX Sequence 735 BP; 191 A; 174 C; 166 G; 204 T; 0 other;
SQ
Query Match 16.1%; Score 183.4; DB 22; Length 735;
Best Local Similarity 78.3%; Pred. No. 4.8e-40;
Matches 220; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
QY 177 TTTTGTCTGTCAACCCAGGCTGAAGTACAGTGGTGTAGCTCAGCGGTCTACTGAGCTTTGA 236
Db 249 TCTCCACGTGTACCCAGGCTAGTGTGAGTGGTAAATCAACATCACTGAGCTTTGA 308
QY 237 CTTCCAGGCTCAAGTGAATCTCTGCTCAGCTTTCCAGTAACTGGGACACAGGCAT 296
Db 309 CTTCTGGGCTCAGGTGATCTCTGCTCAGCTTCCAGCTTCTGAGAGTGGGTATTAGCGT 368
QY 297 GCATCACCAGCTAGGCTATTGTTTACATTTTGTAGAGATGGGTCTCACCATTGTG 356
Db 369 GTGCCAATGTCAGGCTAATTTTGTATTTTGTAGAGATGGGTCTCACCATTGTG 428
QY 357 CCCAGGTTGGTCTCAAACTCTCTGGGCTCAAGCAATCCGCTCAGTCAACCTCCCAATG 416
Db 429 CGCAGGCTGTCTCAAACTCTCTGGGCTCAAGCAATCTCCACCTCAGCTCCCAATG 488
QY 417 CTGGATTACAGCGTGAAGCCACCGGCGGAGCTGAGTAA 457
Db 489 CTGGATTACAGCGTGAAGCCACCGGCGGAGCTGAGTAA 529
RESULT 15
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XX
XX AAK89703;
AC
XX
DT 05-NOV-2001 (first entry)
XX
DE Human digestive system antigen genomic sequence SEQ ID NO: 3279.
XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
XX ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
XX digestive system disorder; Meckel's diverticulum; ds.
XX

OS Homo sapiens.
XX WO200155314-A2.
XX 02-AUG-2001.
XX 17-JAN-2001; 2001WO-US011324.
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
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PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
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PR 05-SEP-2000; 2000US-0229509.
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PR 29-SEP-2000; 2000US-0236370.
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PR 20-OCT-2000; 2000US-0241309.
PR 20-OCT-2000; 2000US-0241326.
PR 01-NOV-2000; 2000US-0244517.
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PR 08-NOV-2000; 2000US-0246475.
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PR 08-NOV-2000; 2000US-0246523.
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PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
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PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
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PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
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PR 17-NOV-2000; 2000US-0249245.
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PR 01-DEC-2000; 2000US-0250160.
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PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
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PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0254097.
XX
XX (HUMA-) HUMAN GENOME SCI. INC.
PA

Tue Jun 10 08:56:17 2003

us-09-617-174c-1.rng

XX Rosen CA, Barash SC, Ruben SM;
PI WPI; 2001-502630/55.
XX Polynucleotides encoding digestive system antigens, useful for
PT diagnosing, treating, preventing and/or prognosing disorders of the
XX digestive system, particularly cancer and cancer metastases -
XX Disclosure; SEQ ID NO 3279; 986pp; English.
XX The present invention provides the protein and coding sequences of a
CC number of human digestive system antigens. These can be used in the
CC diagnosis, treatment and prevention of digestive system disorders,
CC including cancer, Meckel's diverticulum, bacterial or parasitic
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or
CC ulcerative colitis. The present sequence is a genomic DNA fragment
XX encoding a digestive system antigen of the invention.
XX SQ Sequence 735 BP; 191 A; 174 C; 166 G; 204 T; 0 other;
Query Match 16.1%; Score 183.4; DB 22; Length 735;
Best Local Similarity 78.3%; Pred. No. 4.8e-40;
Matches 220; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
Qy 177 TTTTGTCTCTACCCAGGCTGAAGTACAGTGTAGCTCAGGCTCAGTGCAGCTTTGA 236
Db 249 TCTCCCACTGTACCCAGGCTAGTGTGACAGTGTGACAAATCACAACCTCAGTGCAGCTTTGA 308
Qy 237 CCTCCAGGCTCAAGTATCTCTCGTCTCAGCTTTCCAGTAACCTGGGACCAACAGGCAT 296
Db 309 CTTCCTGGGCTCAGGTATCTCTGCTCAGCTCTGAGGAGCTGGGATTATAGCGT 368
Qy 297 GCATCACACGCTAGGCTATTGTTTACATTTTGTAGAGATGGGTCTCACCATGTTG 356
Db 369 GTGCCAACATGTCAGGCTAATTTTGTATTTTGTAGAGATGGGTCTCACCATGCTG 428
Qy 357 CCCAGGTGGTCTCAAACTCTGGGCTCAAGCATCCGCTCAGTCAACCTCCCAAATG 416
Db 429 CGCAGGCTGGTCTCAAACTCTGGACTCAAGCAATCTCCCACTCAGCCTCCAAATG 488
Qy 417 CTGGGATTACAGGCTGAGCCACCGGGCCAGGCTGAGTAA 457
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Search completed: June 7, 2003, 21:08:52
Job time : 442 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 21:08:57 ; Search time 83 Seconds
(without alignments)
4215.882 Million cell updates/sec

Title: US-09-617-174C-1

Perfect score: 1141

Sequence: 1 agataagcacagagagag.....aggataactgtgactccagg 1141

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Gapop 10_0 , Gapext 1.0

Searched: 441362 seqs, 153338391 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

.Listing first 45 summaries

Database :

- Issued Patents NA:**
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4: /cgn2_6/prodata/2/ina/6B COMB.seq**
5: /cgn2_6/prodata/2/ina/PCTUS COMB.seq**
6: /cgn2_6/prodata/2/ina/backfile1.seq**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	178.6	15.7	70000	4	US-09-851-896-3
3	175.8	15.4	36741	4	US-09-301-665-3
4	174.4	15.3	40000	4	US-09-780-049-18
5	173	15.2	1988	2	US-08-257-963B-11
6	173	15.2	1988	4	US-08-367-841A-11
7	173	15.2	1988	5	PCT-US95-07201-11
8	173	15.2	5262	4	US-08-520-373D-5
9	173	15.2	22481	4	US-08-367-841A-43
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11	173	15.2	22484	4	US-09-875-223-2
12	173	15.2	99500	4	US-09-798-096-10
13	172.6	15.1	4421	2	US-08-257-963B-9
14	172.6	15.1	4421	4	US-08-367-841A-9
15	172.6	15.1	4421	4	US-08-520-373D-6
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17	172	15.1	3881	4	US-09-333-593A-1
18	171.8	15.1	81001	4	US-09-750-580-1
19	171.6	15.0	14747	4	US-09-608-285A-42
20	170.8	15.0	15977	4	US-09-608-285A-59
21	170	14.9	246240	2	US-08-724-394A-20
22	170	14.9	246240	2	US-08-724-394A-21
23	170	14.9	246240	2	US-08-724-394A-22
24	169.6	14.9	4285	4	US-09-040-774-1
25	169.4	14.8	1600	2	US-08-487-113D-117
26	169.4	14.8	1600	2	US-08-720-420A-117
27	169	14.8	168575	4	US-09-426-290-1

28	168.6	14.8	20674	4	US-09-641-638-651	Sequence 651, Appl
C 29	168.6	14.8	43950	4	US-09-735-934A-3	Sequence 3, Appli
30	168.6	14.8	111282	4	US-09-754-250-3	Sequence 3, Appli
C 31	168.2	14.7	685	4	US-09-227-357-100	Sequence 10, Appl
C 32	168	14.7	12597	4	US-09-705-299-12	Sequence 12, Appl
C 33	168	14.7	98844	4	US-09-791-211-10	Sequence 10, Appl
C 34	167.8	14.7	112132	4	US-09-741-150-3	Sequence 3, Appli
C 35	167.4	14.7	2477	1	US-08-429-742-1	Sequence 1, Appli
C 36	167.4	14.7	112132	4	US-09-741-150-3	Sequence 3, Appli
37	167	14.6	80246	4	US-09-078-294-4	Sequence 4, Appli
38	167	14.6	80595	4	US-09-078-294-3	Sequence 3, Appli
C 39	166.8	14.6	1460	4	US-09-257-179-23	Sequence 23, Appl
40	166	14.5	72604	4	US-09-268-992-7	Sequence 7, Appli
41	166	14.5	72604	4	US-09-657-474-7	Sequence 7, Appli
C 42	165.8	14.5	70000	4	US-09-851-896-3	Sequence 3, Appli
C 43	165.8	14.5	246240	2	US-08-724-394A-20	Sequence 20, Appl
C 44	165.8	14.5	246240	2	US-08-724-394A-21	Sequence 21, Appl
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RESULT 1
US-08-814-095-7/c
; Sequence 7, Application US/08814095
; Patent No. 6025183
; GENERAL INFORMATION:
; APPLICANT: Soreq, Hermona
; APPLICANT: Zakut, Haim
; APPLICANT: Shani, Moshe
; TITLE OF INVENTION: TRANSGENIC ANIMAL ASSAY SYSTEM FOR
; TITLE OF INVENTION: ANTI-CHOLINESTERASE SUBSTANCES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KOHN & ASSOCIATES
; STREET: 30500 No. 6025183thwestern Highway, Suite 410
; CITY: Farmington Hills
; STATE: Michigan
; COUNTRY: U.S.
; ZIP: 48334
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,095
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Montgomery, Ilene N.
; REGISTRATION NUMBER: 38,972
; REFERENCE/DOCKET NUMBER: 2391.00066
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (248) 539-5050
; TELEFAX: (248) 539-5055
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "Cosmid including ACHS"
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 7q22
; FEATURE:

ALIGNMENTS

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/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 4
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/ NAME/KEY: exon
/ LOCATION: complement (33297..33408)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 5
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/ NAME/KEY: exon
/ LOCATION: complement (32959..33094)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 6
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/ NAME/KEY: exon
/ LOCATION: complement (32569..32628)
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/ OTHER INFORMATION: /number= 7
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (32386..32468)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 8
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (31894..32080)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 9
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/ NAME/KEY: exon
/ LOCATION: complement (31363..31534)
/ OTHER INFORMATION: /gene= "AR"
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/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 11
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/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 12
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/ LOCATION: complement (30470..30626)
/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 13
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/ OTHER INFORMATION: /number= 14
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/ OTHER INFORMATION: /gene= "AR"
/ OTHER INFORMATION: /number= 15
FEATURE:
/ NAME/KEY: exon
/ LOCATION: complement (29664..29856)
/ OTHER INFORMATION: /gene= "ARS"
/ OTHER INFORMATION: /number= 16
/US-08-814-095-7

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	Matches :246;	Conservative	0;	Indels	1;	Gaps
ay	145	CAGAGCTGGGTACTCTTTTTTCTTTTGTCCTGCTACCCAGGCTGAAGTAC	204			
b	8393	CAAATCTATTTTTTTCTTTTAAGGCACAGGGCTCTGCTGTACCAGGCTGTAGTAC	833			
y	205	AGTGGTTTAGCTCACGGCTCACTGCAGCTTTTGACCTCCCAGGCTCAAGTGAATCTCTCTCTGC	264			

Tue Jun 10 08:56:18 2003

us-09-617-174c-1.rni

Accession	Sequence	Length
20204	CCTCCCAAGTTTAAGCAATTCTCTGCGCTCAGCCTCCCAAGTAGCTGTGTACTACAGTCAT	20263
297	GCATCACACGCTAGCGCTATTGTTTTACATTTTGTAGAGTGGGCTCACCATGTTG	356
20264	GCACCACCATGCTAGCTAGTTTTTTTATTTTATGTAGGAGATGGGTTTCACCAAGATG	20323
357	CCACGTTGGTCTCAAATCTCTGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCCAAATG	416
20324	GCAGCGTGCGCTCAAACTCCTGACCTCAAGTGATCGGCCACCTTGGCCTCCCAAAATG	20383
417	CTGGGATTAACGGCGTGAACCAACCGGCCGACG	448
20384	CTGGGATTAACAGTGTGAGCCACCGGCGCTGG	20415

RESULT 5
US-08-257-963B-11
; Sequence 11, Application US/08257963B
; Patent No. 5840686
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Becerra, S.
; APPLICANT: Patricia; Schwartz, Joan P.;
; APPLICANT: Taniwaki, Takayuki
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION OF ITS NOVEL
; TITLE OF INVENTION: BIOLOGICAL ACTIVITY AND SEQUENCES ENCODING
; TITLE OF INVENTION: AND EXPRESSING THE PROTEIN
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1988 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Human
FEATURE:
NAME/KEY: JT108
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 2 kb PCR product using
OTHER INFORMATION: primers, SEQ ID: 13 and 14.
US-08-257-963B-11.

Query Match 15.2%; Score 173; DB 2; Length 1988;
Best Local Similarity 68.3%; Pred. No. 7.6e-40;

	Matches	250;	Conservative	0;	Mismatches	115;	Indels	1;	Gaps	1
QY	98	TGGGAACACAGGAGGACAAGAACAGGCTCCACGAAGAGATTTCAGACGACGAGCTGCGTAC	157							
Db	489	TGGGTTCCACAGGGGAACATAACCACTCACCTACACAGAATAGTCTCTTTTTTTTTTTTTTTT	548							
QY	158	TCCTTTTTCTTTTTTGTTTTCTTTTGTCTCTGTCAACCAGGCTGAAGTACAGTGGTGTAGCTCA	217							
Db	549	TNNNTCTTCTGACACGGAGTCTGCTPTTGTCTNCCAAAGGCTGGAGTGGCACTGGTGTGATCT	608							
QY	218	CGGCTCACTCGAGCTTTGACCTCCCAAGGCTCAAGTGATCCTCTCGTCTCAGCTTTTCCAAAG	277							
Db	609	CAGCTCACTGGAACCTCTGCCTCCCTGGTTCAAGGAAATTCCTCCTCCCTCAGCCTCCAGAG	668							
QY	278	TAACTGGGACACAGGCAATGCATCAACACGTAGGCTATGTTTTTACATATTTTTTGTAGAG	337							
Db	669	TAGCTGGGATTTACAGGCACCTGCGCATCATGCCCCAGCTAAT-TTTTGTATTTTTTAGTAGAG	727							
QY	338	ATGGGGTCTCACCATGTTGCCAGGTTGGTCTCAAACTCCTCGGGCTCAAGCAATCCGGTCTC	397							
Db	728	ACGGGGTTTCAACATGTTGCTTAGGCTGGTCTCTCAAACTCCCGGGCTCAAGCGATCCACCC	787							
QY	398	ACGTCAACCTCCCCAAATGCTGGGATTTACAGCGTGCAGCCACCGGCGCAGGGCTGAGTAA	457							
Db	798	GCTTGGCTCCCAAAGTCTGGGATTTACAGGGGTGAGCCACCGCGCTGGCCAGAAATAA	847							
QY	458	TCCTAA	463							
Db	848	TCCTAA	853							

RESULT 6
US-08-367-841A-11
; Sequence 11, Application US/08367841A
; Patent No. 6319687
; GENERAL INFORMATION:
; APPLICANT: Chader, Gerald J.; Rodriguez,
; APPLICANT: Ignacio R.; Mazuruk, Krzysztof;
; APPLICANT: Tombran-Tink, Joyce
; TITLE OF INVENTION: PIGMENT EPITHELIUM
; TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
; TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan
; STREET: 345 Park Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/367,841A
; FILING DATE: 30-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/257,963
; FILING DATE: 07-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/952,796
; FILING DATE: 24-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: DOROTHY R. AUTH
; REGISTRATION NUMBER: 36434
; REFERENCE/DOCKET NUMBER: 20264126US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 11:

Sequence 5, Application US/08520373D
Patent No. 6451763
GENERAL INFORMATION:
APPLICANT: Tombran-Tink, Joyce
APPLICANT: Steele, Fintan R
APPLICANT: Chader, Gerald J
APPLICANT: Becerra, Sofia P
APPLICANT: Johnson, Lincoln V
APPLICANT: Rodriguez, Ignacio R
TITLE OF INVENTION: RETINAL PIGMENTED EPITHELIUM DERIVED NEUROTROPIC FACTOR
FILE REFERENCE: 2026-4203US1
CURRENT APPLICATION NUMBER: US/08/520,373D
CURRENT FILING DATE: 1995-08-29
PRIOR APPLICATION NUMBER: 08/377,710
PRIOR FILING DATE: 1995-01-25
PRIOR APPLICATION NUMBER: 08/279,979
PRIOR FILING DATE: 1994-07-25
PRIOR APPLICATION NUMBER: 07/894,215
PRIOR FILING DATE: 1992-06-04
PRIOR APPLICATION NUMBER: 07/952,796
PRIOR FILING DATE: 1992-09-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 5262
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
OTHER INFORMATION: EXON 35-161; EXON 1142-1297; EXON 1984-2187;
OTHER INFORMATION: EXON 5170-5255; INTRON 162-1141; INTRON
OTHER INFORMATION: 1298-1983; INTRON 2188-5169; CDS 35-161; CDS
OTHER INFORMATION: 1142-1297; CDS 1984-2187; CDS 5170-5255
NAME/KEY: exon
LOCATION: (35)..(160)
NAME/KEY: exon
LOCATION: (1142)..(1297)
NAME/KEY: exon
LOCATION: (1984)..(2187)
NAME/KEY: exon
LOCATION: (5170)..(5256)
NAME/KEY: intron
LOCATION: (162)..(1141)
NAME/KEY: intron
LOCATION: (1298)..(1983)
NAME/KEY: intron
LOCATION: (2188)..(5169)
OTHER INFORMATION: n = a or g or t or c, any base

US-08-520-373D-5
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Best Local Similarity 68.3%; Pred. No. 1.3e-39;
Matches 250; Conservative 0; Mismatches 115; Indels 1; Gaps 1;
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DB 521 TGGGTTACAGGGGAACTAATACGAGCTCACTACAGATATCTTTTTTTTTTTTTTT 580
QY 158 TCCTTTTCTTTTCTTTTCTGCTGTGCTCACCAGGCTCAAGTACAGTGTAGCTCA 217
DB 581 TNNNCTTCTGAGACGGAGTCTCGCTTTGTGTCNCAAGCTGGAGTGGTGTGTCT 640
QY 218 CGGCTCACTGAGCTTTTTCAGCTCCAGGCTCAAGTGTCTCTGCTCAGCTTTTCAAG 277
DB 641 CAGCTCACTGCAACTCTGCTCTCCCTGCTTCAAGGAATCTCTGCTCAGCTCCAG 700
QY 278 TAACTGGGACCAAGGATGATCATCACCAGCTAGCTATGTTTACATTTTGTGAG 337
DB 701 TAGCTGGGATTACAGGACCTGCTCCATCATGCCAGCTAAT-TTTTGTATTTTAGTAG 759
QY 338 ATGGGGTCTCACCATTGTTGCCAGGTTGGTCTCAACTCTGGGCTCAAGCAATCCGCTC 397
DB 760 ACGGGGTTTACCATTGTTGCTTAGGCTGTCTCAAAACTCCCGGGCTCAAGCAATCCACC 819

QY 398 ACGTCAACCTCCCAAAATGCTGGATTACAGGCTGAGCCACCGGGCCAGGCTGAGTAA 457
DB 820 GCCTTGGCTCCCAAAAGTCTGGATTACAGGCTGAGCCACCGGGCTGSCCAGATAA 879
QY 458 TCCTAA 463
DB 880 TCTTAA 885
RESULT 9
US-08-367-841A-43
Sequence 43, Application US/08367841A
Patent No. 6319687
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Rodriguez, Ignacio R.; Mazuruk, Krzysztof;
APPLICANT: Tombran-Tink, Joyce
TITLE OF INVENTION: PIGMENT EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARACTERIZATION GENOMIC
TITLE OF INVENTION: ORGANIZATION AND SEQUENCE OF THE PEDF GENE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/367,841A
FILING DATE: 30-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/257,963
FILING DATE: 07-JUN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US2
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 22481 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
FEATURE:
NAME/KEY: P1-147
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: full length genomic
OTHER INFORMATION: sequence for PEDF plus flanking sequences.
US-08-367-841A-43
Query Match 15.2%; Score 173; DB 4; Length 22481;
Best Local Similarity 68.3%; Pred. No. 2.9e-39;
Matches 250; Conservative 0; Mismatches 115; Indels 1; Gaps 1;
QY 98 TGGGAAGACAGGAGGACAGAGGCTCCACGAGAGATTTCAGAGCAGAGCTGCGTAC 157
DB 15086 TGGGTTACAGGGGAACTAATACGAGCTCACTACAGATATCTTTTTTTTTTTTTTT 15145

401 TC AACCTTCCCCAATGCTGGATTACAGGCGTGAGCCACCGGGCCAGGCGCTGA 453

RESULT 13

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US-08-257-963B-9
Sequence 9, Application US/08257963B
Patent No. 5840686
GENERAL INFORMATION:
APPLICANT: Chader, Gerald J.; Becerra, S.
APPLICANT: Patricia; Schwartz, Joan P.;
APPLICANT: Taniwaki, Takayuki
TITLE OF INVENTION: PRIMED EPITHELIUM
TITLE OF INVENTION: DERIVED FACTOR: CHARA
TITLE OF INVENTION: BIOLOGICAL ACTIVITY A
TITLE OF INVENTION: AND EXPRESSING THE PR
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/257,963B
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/952,796
FILING DATE: 24-SEPT-1992
ATTORNEY/AGENT INFORMATION:
NAME: DOROTHY R. AUTH
REGISTRATION NUMBER: 36434
REFERENCE/DOCKET NUMBER: 20264126US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 4421 Base Pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Unknown
MOLECULE TYPE: Genomic DNA
ORIGINAL SOURCE:
ORGANISM: Human
FEATURE:
NAME/KEY: JT101
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: 7.1 kb Bam HI
OTHER INFORMATION: fragment Derived fr
OTHER INFORMATION: genomic DNA

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US-08-257-963B-9
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Best Local Similarity 69.3%; Pred. No. 1.5e-39;
Matches 235; Conservative 0; Mismatches 104; Indels 0; Gaps 0;

QY    149  GTCGGTACTCCTTTTCTTTTGCTGTCGTCAACCCAGGCGTAAGTCAAGTG 208
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Db     3788 GCCTCTATTATTTTTTTTGAGATGGAGTCTCACACTGTCACCTGGCGCTGGAGTGCAGTG 3847

QY    209  GTTAGCTACGGCTCACTGCAGCTTTGACTCCCAGGCTCAAAGTGATCCTCTCGTCTCAG 268
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db     3848 GAGCGCATCTCGGCTCACTGCACACCTCCGCCCTCTCTGGGTTCAAGAGATTTCTCTGCCTCAG 3907
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Query Match	15.2%	Score 173;	DB 4;	Length 22484;
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y	98	TGGGAAGACAGGAGGACAAAGACAGGCTCCACCAAGAGATTTCCAGACGACGCTGCGTAC	157	
b	15086	TGGGTTCCACAGGGGAACATAACCAGCTCACTACAGAAATAGTCTTTTTTTTTTTTTTTTT	15145	
y	158	TCCTTTTCTTTTGTCTTTTCTCTCTGTCAACCAGGCTTGAGTACAGTGGTTAGCTCA	217	
b	15146	TNNCTTTCTGACACGGAGCTCGCTTTGTGTCNCAAGGCTGGAGTGCAGTGGTGTGATCT	15205	
y	218	CGGCTCACTCGAGCTTTGACCTCCACGAGCTCAAGTGATCTCTCGTCTCAGACTTCCAAAG	277	
b	15206	CAGCTCACTGCAACTCTGCTCCCTGGTTCAGGAATTCCTCGCTCAGGCTCCAGAG	15265	
y	278	TAACTGGGACACACAGGCGATGCATCACCAAGCTAGGCTATTGTTTTTACATTTTTTGTAGAG	337	
b	15266	TAGCTGGGATTACAGGCACCTGCCATCATGCCCAAGCTAAAT-TTTTGTATTTTTTATAGAG	15324	
y	338	ATGGGGTCTACCATGTTGCCCAGGTTGGTCTCAAACTCCCTGGGCTCAAGCAATCCGCTC	397	
b	15325	ACGGGGTTTACCATGTTGCCCTAGGCTGGTCTCAAACTCCCGGGCTCAAGCGATCCACCC	15384	
y	398	ACGTCMAACTCCCAAAATGCTGGGATTACAGGCGTGTAGCCACCGGGCGAGGCTGAGTAA	457	
b	15385	GCCTTGGCTCCCAAGTCTGGGATTACAGGCGTGTAGCCACCGGGCGTGCACAGATAA	15444	
y	458	TCCTAA 463		
b	15445	TCTTAA 15450		

RESULT 12

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US-09-798-096-10
; Sequence 10, Application US/09798096
; Patent No. 6395378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODUL
; FILE REFERENCE: RTS-0207
; CURRENT APPLICATION NUMBER: US/09/7
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 99500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; US-09-798-096-10

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	Query Match	15.2%	Score 173;	DB 4;	Length 99500;
	Best Local Similarity	74.4%;	Pred. NO. 6.6e-39;		
	Matches 218;	Conservative	0;	Mismatches. 75;	Indels 0; Gaps 0;
QY	161	TTTTTCTTTTGTCTTTCTGTCACCCAGGCTCAAGCTACAGTGGTTAGCTCACGG	220		
DB	35956	TTTTTTTTTGAGACAGTCTCGCTCTGTCCAGGCTGGAGTGAAGTGGTATGATCTGG	36015		
QY	221	CTCACTGCAGCTTTTGACCTCCAGGCTCAAGTGATCTCTCGTCTCAGCTTTCAGATTA	280		
DB	36016	CTCACTGCAGCTCCACCTCCGGGTTCAGGTGATCTTGTCCTCAGCCTCCAGGTAG	36075		
QY	281	CTGGGACACAGGCATGCATCACCAGCTAGGCTATTCTTTACATTTTTTGTAGAGATG	340		
DB	36076	CTGGAACTACAGTGCACACCACTGCTCGCTAAATTTTTTGTATTTTCAGTGAACG	36135		
QY	341	GGGTCTCACATGTTGCCAGGTTGGTCTCAAACCTCTGGGCTCAAGCAATCCCGCTCACG	400		
DB	36136	AGGATTTTTCCTCTGCTCTGAGCTAGTCTTTGAACCCCTGAGCTCAGGCAATCCGCCGCC	36195		


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QY 209 GTTAGCTACGGCTCACTGCAGCTTTGACCTCCAGGCTCAAGTGATCCTCTCGTCTCAG 268
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 3848 GAGCGATCTCGGCTCACTGCAACCTCCGCTCCTGGTTCAAGAGATTCTCTGCTCAG 3907
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 269 CTTTCCAAGTAACTGGGACCAAGGATGATCATCACAGCTAGGCTATTGTTTACATTT 328
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 3908 CTTCCCAAGTAGTGGGATTACAGTGCCCAACCAAGCTGGCTAGTTTGTGATTT 3967
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 329 TTTGTAGAGATGGGCTCTCACCATTGTGCCAGGTTGGTCTCAAACTCTGGGCTCAAGC 388
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 3968 TTAGTAAAGATGGGTTTCAACCATGTTGCCAGGCTGGTCTTGAACCTCTGACATCAGGT 4027
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 389 AATCCGCTCAGTCAACCTCCCAATGCTGGGATTACAGGCTGAGCCACCGGCCAGG 448
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 4028 GATCCGCCACCTTAGCCTCCCAAGTGTGGGATTACAGGCTGAGCCACCATACCTGG 4087
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 449 GCTGACTAATCCTAATCACAGGATTTTAAAAAGAACTT 487
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 4088 CCAGCAAAACCTCTTTAACTTGTTGTTCCATGGGCTCCTT 4126
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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Search completed: June 7, 2003, 22:26:35
Job time : 189 secs

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	190.2	16.7	66804	10	US-09-740-041-3	Sequence 3, Appli
c	185.4	16.2	916	9	US-09-764-891-8218	Sequence 8218, Ap
2	183.4	16.1	735	9	US-09-764-891-8245	Sequence 8245, Ap
c	182	16.0	288	9	US-10-115-278-1	Sequence 1, Appli
3	181.4	15.9	174424	10	US-09-967-768A-314	Sequence 314, App
c	180	15.8	21470	9	US-10-092-154-1157	Sequence 1157, Ap
4	180	15.8	21470	10	US-09-764-847-1157	Sequence 1157, Ap
c	179.8	15.8	1423	9	US-09-796-753-97	Sequence 97, Appl
c	179.8	15.8	1423	9	US-09-796-753-111	Sequence 111, Appl
c	179.8	15.8	1440	12	US-10-067-422-6	Sequence 6, Appli
5	179	15.7	7233	9	US-10-091-504-2123	Sequence 2123, Ap
c	179	15.7	7233	10	US-09-764-869-2123	Sequence 2123, Ap
c	178.6	15.7	1125	9	US-10-091-438-77	Sequence 77, Appl
c	178.6	15.7	1125	10	US-09-764-853-209	Sequence 209, App
6	178.6	15.7	20190	9	US-09-996-015-3	Sequence 3, Appli
c	178.6	15.7	66804	10	US-09-740-041-3	Sequence 3, Appli
7	178.4	15.6	16181	9	US-10-092-154-1426	Sequence 1426, Ap
c	178.4	15.6	16181	9	US-09-764-891-6956	Sequence 6956, Ap
8	178.4	15.6	16181	10	US-09-764-847-1426	Sequence 1426, Ap
c	178.4	15.6	16181	10	US-09-764-847-1426	Sequence 1426, Ap

Query Match	16.7%	Score 190.2	DB 10	Length 66804
Best Local Similarity	70.2%	Pred. No. 1.1e-46		
Matches 255	Conservative 0	Mismatches 108	Indels 0	Gaps 0
QY	86	ATGAAGAGCTGTGGGAAGACAGCAGGACACAGACAGGCTCCACGAAGAGATTTCAGAGC	145	
Db	45572	ATTCAAGAGCTGAATGAGACAGCAGGCCCTCTGCCATCTGGAATTTAAATTGTTTCACCCC	45631	
QY	146	AGAGCTGCGTACTCCTCTTTCTTTTGTGTTCTTTGTCTGTCTACCCAGGCTGAAGTACA	205	
Db	45632	TCACCTTTTTTTTTTTTTTTTTTTTTTGTATCAGTCACCTGTCTACCCAGGCTGGAGTGCA	45691	
QY	206	GTGGTTAGCTCAGCGCTCAGTCAGCTTTGACCTCCAGAGCTCAAGTGATCCTCTCGTCT	265	
Db	45692	GTGGTGAGATCTTGCTCTACTGCAACCTCGCCCTCACGGGTTCAAGCAATTCCTCGTCCCT	45751	
QY	266	CAGCTTTTCCAAGTAACTGGGACACAGGATGATCACCAGCTAGAGCTATTGTTTATACA	325	
Db	45752	CAGCGGCCAAGTAGCTGGGATTAAGCAGCGGCCACCATGCCAGGCTAAATTTTTTGTA	45811	
QY	326	TTTTTTGTAGAGATGGGGTCTCACCATGTTGCCCAGGTTGGTCTCTCAAACCTCCTGGGCTCA	385	

Db 45812 TTTTGTAGATGGGGTTTGTCTATGTGTGACCGAGGTGCTTGAACCTCTGCGCTCA 45871
 QY 386 AGCAATCCGCTCAGGTCAACCTCCCAATGCTGGGATTACAGGGGTGAGCCACCGGCC 445
 Db 45872 AGTATCTGTCCACCTCAGCTCCCAAGTGTAGGATTACAGGTGTGAGCCACCGTCC 45931
 QY 446 AGG 448
 Db 45932 TGG 45934

RESULT 2

US-09-764-891-8218/c
 ; Sequence 8218, Application US/09764891
 ; Publication No. US20030077808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC006
 ; CURRENT APPLICATION NUMBER: US/09/764,891
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 10231
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 8218
 ; LENGTH: 916
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-891-8218

Query Match 16.2%; Score 185.4; DB 9; Length 916;
 Best Local Similarity 75.2%; Pred. No. 2.1e-46; Indels 0; Gaps 0;
 Matches 231; Conservative 0; Mismatches 76;
 QY 177 TTTTGTCTGTCAACCCAGGTGAAGTACAGTGTAGTCTCAGCGCTCACTGCGCTTTGA 236
 Db 911 TCTCACTGTCTACCCAGGTGGAGTGCAGTGCATGATCCCGCTCAGCGCAACCTGTG 852
 QY 237 CCTCCAGGTCAAGTATCTCTGCTCAGCTTCCAGTAACTGGGACCCACGAGCAT 296
 Db 851 CCTCTGGTTCAGTGAATCTCTGCTCAGCTCCCAAGTACCTGGGACCCACGAGTGC 792
 QY 297 GCATCACACGCTAGGTATTTTGTATTTTGTAGAGATGGGTCTCACCATTGTTG 356
 Db 791 ACATCACACACCTGGCTTAATCTTTGTATTTGTAGATGGGTCTCACCATTGTTG 732
 QY 357 CCCAGGTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAATG 416
 Db 731 GCCAGGTGGTCTCAAACTCTGGGCTCAAGTATCCGCTCAGCTCAACCTCCCAATG 672
 QY 417 CTGGGATTACAGGTGTGAGCCACCGGCTGAGTAACTCTCAATCAATCAAGATTTA 476
 Db 671 CTGGGATTATAGGCGGAGCCACCGGCTGAGTAACTCTCAATCAATCAAGATTTA 612
 QY 477 AAAAGAA 483
 Db 611 AAATPAA 605

RESULT 3

US-09-764-891-8245
 ; Sequence 8245, Application US/09764891
 ; Publication No. US20030077808A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PC006
 ; CURRENT APPLICATION NUMBER: US/09/764,891
 ; CURRENT FILING DATE: 2001-01-17
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 10231
 ; SOFTWARE: Patent in Ver. 2.0
 ; SEQ ID NO 8245

; LENGTH: 735
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-764-891-8245
 Query Match 16.1%; Score 183.4; DB 9; Length 735;
 Best Local Similarity 78.3%; Pred. No. 7.6e-46;
 Matches 220; Conservative 0; Mismatches 61; Indels 0; Gaps 0;
 QY 177 TTTTGTCTGTCAACCCAGGTGAAGTACAGTGTAGTCTCAGCGCTCACTGCGCTTTGA 236
 Db 249 TCTCCCACTGTACCCAGGTAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 308
 QY 237 CCTCCAGGTCAAGTATCTCTGCTCAGCTTTCAGTAACTCTGGGACCCACGAGCAT 296
 Db 309 CTTCCTGGCTCAGGTATCTCTGCTCAGCTCCTGAGGAGCTGGGATATAGGCGT 368
 QY 297 GCATCACACGCTAGGTATTTTGTATTTTGTAGAGATGGGTCTCACCATTGTTG 356
 Db 369 GTGCCAATGTCTCAGGTAAATTTTGTATTTTGTAGAGATGGGTCTCACCATTGTTG 428
 QY 357 CCCAGGTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAATG 416
 Db 429 CGCAGGTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAATG 488
 QY 417 CTGGGATTACAGGTGTGAGCCACCGGCTGAGTAACTCTCAATCAATCAAGATTTA 457
 Db 489 CTGGGATTAGAGGTGTGAGCCACTGTGCCACGCGCAAGTAA 529

RESULT 4

US-10-115-278-1/c
 ; Sequence 1, Application US/10115278
 ; Publication No. US20030082644A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Schuetz, Ekkehard
 ; APPLICANT: Urnovitz, Howard B.
 ; APPLICANT: Chronix Biomedical, Inc.
 ; TITLE OF INVENTION: Diagnostic Detection of Nucleic Acids
 ; FILE REFERENCE: 018651-000320US
 ; CURRENT APPLICATION NUMBER: US/10/115,278
 ; CURRENT FILING DATE: 2002-07-09
 ; PRIOR APPLICATION NUMBER: US 60/280,523
 ; PRIOR FILING DATE: 2001-03-30
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 288
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: AluJ consensus
 ; OTHER INFORMATION: sequence
 US-10-115-278-1

Query Match 16.0%; Score 182; DB 9; Length 288;
 Best Local Similarity 81.4%; Pred. No. 1.1e-45; Indels 1; Gaps 1;
 Matches 223; Conservative 0; Mismatches 50;
 QY 177 TTTTGTCTGTCAACCCAGGTGAAGTACAGTGTAGTCTCAGCGCTCACTGCGCTTTGA 236
 Db 273 TCTCGCTCTGTCCGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 214
 QY 237 CCTCCAGGTCAAGTATCTCTGCTCAGCTTTCAGTAACTCTGGGACCCACGAGCAT 296
 Db 213 CCTCCCGGCTCAAGGATCTCTGCTCAGCTCCCGAGTAGTCTGGGACTACAGGCGC 154
 QY 297 GCATCACACGCTAGGTATTTTGTATTTTGTAGAGATGGGTCTCACCATTGTTG 356
 Db 153 GCGCCACCAACGCGCGCTAAAT-TTTTGTATTTTGTAGAGCGGGTTTCACTATGTTG 95
 QY 357 CCCAGGTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAATG 416

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Db 94 CCCAGGCTGGTCTCGAATCTCTGGGCTCAAGTGATCTCCCGCTCGGGCTCCCAAGTG 35
QY 417 CTGGGATTACAGCGCTGAGCCACCGGGCCAGGGC 450
Db 34 CTGGGATTACAGCGCTGAGCCACCGGGCCCGGCC 1

RESULT 5
US-09-967-768A-314/c
; Sequence 314, Application US/09967768A
; Patent No. US20020150877A1
; GENERAL INFORMATION:
; APPLICANT: Augustus, Meena
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-72
; CURRENT APPLICATION NUMBER: US/09/967,768A
; CURRENT FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,109
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,034
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,111
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 325
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 314
; LENGTH: 174424
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-967-768A-314

Query Match 15.9%; Score 181.4; DB 10; Length 174424;
Best Local Similarity 77.6%; Pred. No. 1e-43;
Matches 232; Conservative 0; Mismatches 66; Indels 1; Gaps 1;

QY 177 TTTTGTCTGTCAACGAGCTGAAGTACAGTGTAGCTCACGGCTCACTGAGCTTTGA 236
Db 154673 TCTGGCTGTCACTCAGGCTGGAGTGCAAGTGTGGATCATGTGCTCACTGCAACCTGA 154614

QY 237 CTTCCAGGCTCAAGTATCTCTGCTCAGCTTCCAGTAACTGGGACACAGGCAT 296
Db 154613 CTTCCAGGTTCAAGTATCTCTCCCACTCAGCTCCCGAGGCTGGGACTACAGATG 154554

QY 297 GCATCACCAGCTAGGCTATTGTTTACATTTTGTAGAGATGGGCTCTCACCATTG 356
Db 154553 GTGCCACACGCGCGCTAAATTTTAA-TTTTTGTAGAGATGGGCTCTCATTATG 154495

QY 357 CCCAGTTGGTCTCAAACTCTCTGGGCTCAAGCAATCCGCTCAGTCAACCTCCCCAAATG 416
Db 154494 CCCAGGCTGGTCTCAAACTCTTGACCTCAGGTGATCCACCTGCCTCGACCTCCCAAGTG 154435

QY 417 CTGGGATTACAGCGCTGAGCCACCGGGCCAGGGCTGAGTAATCTTAATCAGGATTTT 475
Db 154434 CTGGGATTACAGCGCTGAGCCACCGGGCTGAAATGACCTTTTAAATAATGTT 154376

RESULT 6
US-10-092-154-1157
; Sequence 1157, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1157
; LENGTH: 21470
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-10-092-154-1157

Query Match 15.8%; Score 180; DB 9; Length 21470;
Best Local Similarity 72.2%; Pred. No. 7.3e-44;
Matches 234; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 135 GATTTTCAGACGAGCTGGTACTCTCTTTTCTTTTGTGTTTCTTTTGTCTGTGCAAGTGA 194
Db 1585 GAGGTGACTGAAGAATTTTGTGTTTGTGAGACGGAGTCTTGCTCTGTGCAAGTGA 1644

QY 195 GCTGAAGTACAGTGGTTAGCTCAGCGCTCAGTGCAGCTTTGACCTCCAGGGCTCAAGTGA 254
Db 1645 GCTGAGTGCAGTGGCGTGATCTTGCTCAGTGCATCTCCGCTCCAGGGCTCAAGCGA 1704

QY 255 TCCTCTCGTCTCAGCTTTTCCAAAGTAACTGGGACACAGCATGTCACACGCTAGGCT 314
Db 1705 TTCTCTCGCTCAGGCTCTGAGTAACTGGGATTCAGGTGCACACACGCTGGCT 1764

QY 315 ATTGTTTACATTTTGTAGAGATGGGCTCTCAGCATGTTGCCAGGTTGGTCTCAAAAC 374
Db 1765 AATTTTGTATTTTGTAGTAGACAGGCTTTTCAAAATGTTGCCAGGCTGGTCTCAAAAC 1824

QY 375 TCCTGGGCTCAAGCAATCCGCTCAGTCAACCTCCCAAAATGCTGGGATTCAGGCGTGA 434
Db 1825 TCCTGACCTCAAGTGTGCGCGGCTCGGCTCCCAAAAGTCTGGGATTCAGGTTGTA 1884

QY 435 GCCACGGCGGCGGCTGAGTAAT 458
Db 1885 GCCACTGTGCTGGCTGAAATAAT 1908

RESULT 7
US-09-764-847-1157
; Sequence 1157, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1157
; LENGTH: 21470
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1157

Query Match 15.8%; Score 180; DB 10; Length 21470;
Best Local Similarity 72.2%; Pred. No. 7.3e-44;
Matches 234; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 135 GATTTTCAGACGAGCTGGTACTCTCTTTTCTTTTGTGTTTCTTTTGTCTGTGCAAGTGA 194
Db 1585 GAGGTGACTGAAGAATTTTGTGTTTGTGAGACGGAGTCTTGCTCTGTGCAAGTGA 1644

QY 195 GCTGAAGTACAGTGGTTAGCTCAGCGCTCAGTGCAGCTTTGACCTCCAGGGCTCAAGTGA 254
Db 1645 GCTGAGTGCAGTGGCGTGATCTTGCTCAGTGCATCTCCGCTCCAGGGCTCAAGCGA 1704

QY 255 TCCTCTCGTCTCAGCTTTTCCAAAGTAACTGGGACACAGCATGTCACACGCTAGGCT 314
Db 1705 TTCTCTCGCTCAGGCTCTGAGTAACTGGGATTCAGGTGCACACACGCTGGCT 1764

QY 315 ATTGTTTACATTTTGTAGAGATGGGCTCTCAGCATGTTGCCAGGTTGGTCTCAAAAC 374
Db 1765 AATTTTGTATTTTGTAGTAGACAGGCTTTTCAAAATGTTGCCAGGCTGGTCTCAAAAC 1824

QY 375 TCCTGGGCTCAAGCAATCCGCTCAGTCAACCTCCCAAAATGCTGGGATTCAGGCGTGA 434
Db 1885 GCCACTGTGCTGGCTGAAATAAT 1908
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1825 TCTGACCTCAAGTGTCCGCCGCTCGGCTCCCAAGTCTCGGATTACAGTGTGA 1884

435 GCCACCGGCCAGGGCTGAGTAAT 458
1885 GCCACTGTGCTGGCTGAATAT 1908

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (31)...(444)
US-09-796-753-97

Query Match 15.8%; Score 179.8; DB 9; Length 1423;
Best Local Similarity 76.7%; Pred. No. 1.5e-44;
Matches 220; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 177 TTTTGCTCTGTCAACCCAGGCTGAAGTACAGTGGTTAGCTCAGCGCTCACTGCAGCTTTGA 236
DB 1385 TCTCACTCTGTCAACCCAGGCTGGAGTACGGTGTATGATCAGAGCTCACTGCAGCTCTTA 1326
QY 237 CCTCCAGGCTCAAGTGATCTCTCGTCTCAGCTTTTCCAAAGTAACTGGGACCAAGCAT 296
DB 1325 CTTCCAGGCTCAAGTGATCTCTCACTTCAAGCTCCCTTTGTAGTGGGACCAAGGTGC 1266
QY 297 GCATCACCAAGCTAGGCTATTTTATCATTTTGTAGATGGGTCTCACCATTGTG 356
DB 1265 GTGCCACCACTTGGCTAAATTTTAAATTTTGTAGATGGGTCTTGTCTATGTG 1206
QY 357 CCCAGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCACTCAACTCCCAAAATG 416
DB 1205 CCCAGGCTGGTCTCAAAATTTCTGGGCTCAAGTGTCTTTTCCGCTCAGCTCCCAAGTG 1146
QY 417 CTGGGATTACAGGCTGAGCCACCGGGCCAGGGCTGAGTAATCTCTAA 463
DB 1145 CTGGGACTACAGACATGAGCTACTGCGCCAGGCTTAGAAAACTTA 1099

RESULT 9
US-09-796-753-111/c
Sequence 111, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/336,536
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/365,164
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/399,723
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/409,634
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/471,179
PRIOR FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 09/474,071
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/514,010
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/516,745
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: 09/597,993
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/630,334
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 97
LENGTH: 1423
TYPE: DNA

US-09-796-753-97/c
Sequence 97, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09796,753
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR APPLICATION NUMBER: 09/223,094
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/223,546
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/224,246
PRIOR FILING DATE: 1998-12-30
PRIOR APPLICATION NUMBER: 09/259,388
PRIOR FILING DATE: 1999-02-26
PRIOR APPLICATION NUMBER: 60/122,458
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 09/312,359
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: 09/336,536
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 09/342,687
PRIOR FILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: 09/345,464
PRIOR FILING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: 09/365,164
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 09/399,723
PRIOR FILING DATE: 1999-09-20
PRIOR APPLICATION NUMBER: 09/409,634
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: 09/471,179
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PRIOR APPLICATION NUMBER: 09/474,071
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/474,072
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: 09/514,010
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 09/516,745
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/572,002
PRIOR FILING DATE: 2000-05-14
PRIOR APPLICATION NUMBER: 09/597,993
PRIOR FILING DATE: 2000-06-19
PRIOR APPLICATION NUMBER: 09/599,596
PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION NUMBER: 09/630,334
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: 09/606,565
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/606,317
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: 09/665,666
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/677,751
PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
SEQ ID NO 97
LENGTH: 1423
TYPE: DNA


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; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/131,672
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/130,693
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 1440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-067-422-6

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Query Match 15.8%; Score 179.8; DB 12; Length 1440;
Best Local Similarity 76.7%; Pred. No. 1.5e-44;
Matches 220; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

Qy	177	TTTTGCTCTGTCA	CCAGGCTGAAGTAC	AGTGTGTAGCTC	ACGGCTCACTGC	AGCTTTGA	236
Db	1412	TCTCACTCTGTCA	CCAGGCTGGAGTAC	GGTGTTCATGAT	CAGAGCTCACTGC	AGCCCTCTA	1353
Qy	237	CCTCCCAAGGCT	CAAGTGATCCTCT	CGTCTCAGGCTT	TCCAAGTAACTGGG	ACCACAGGCAAT	296
Db	1352	CCTTCCAGGCT	CAAGTGATCCTCT	CACCTTCAAGCGT	CCCTTGTAGCTGGG	ACCACAGGTGC	1293
Qy	297	GCATCAACCA	CGGTAGGCTATGT	TTTTTACATTTTT	TGTAGAGATGGGGT	CTCAACAATGTTG	356
Db	1292	GTGCCACCA	CACATCTGGCTAAT	TTTTTTTAAATTTTT	TGTAGAGATGGGGT	CTTGTGATATGTTG	1233
Qy	357	CCACGGTTGTG	TCTCAAACTCCT	GGGCTCAAGCAAT	CCGGCTACGTC	CAACTCCCCAAATG	416
Db	1232	CCACAGGCTGT	CTCAAAATTCCT	GGGCTCAAGTGCT	TCTTTTCGGCT	CAGCCTCCCAAGATG	1173
Qy	417	CTGGGATTCAG	CGGTGAGCCAC	CGGGCCAGGCT	CTAGTAACTCCT	ATAA	463
Db	1172	CTGGGACTAC	GACATCAGCTACT	CTGGGCCCAGGCT	TTAGAAAACTTTA		1126

```

RESULT 11
US-10-091-504-2123/c
; Sequence 2123, Application US/10091504
; Publication No. US2003005968A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C1
; CURRENT APPLICATION NUMBER: US/10/091,504
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2123
; LENGTH: 7233
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-091-504-2123

```

Query Match 15.7%; Score 179; DB 9; Length 7233;
Best Local Similarity 77.6%; Pred. No. 7.4e-44;
Matches 229; Conservative 0; Mismatches 65; Indels 1; Gaps 1;

Qy	158	TCCTTTTCTTTTGTGTTCTTTTGTCTGTGTCACCCAGGCTGAAGTACAGTGGTTAGTCTCA	217
Db	3492	TCCTTTCTTTGAGAGGGTTTTATTCTGTCAACCCAGGCTGGAGTGCAGTGGCACGATCA	3433
Qy	218	CGGCTCACTGCAGCTTTGACTCCCAAGGCTCAAGTGATCTCTCGTCTCAGCTTCCCAAG	277
Db	3432	GGGCTCACTGCAGCTCGACTCTCGGCTCAAGTGATCTCTGCTCAGCTCCCAAG	3373
Qy	278	TAACTGGGACCAAGGCTGATCACCACGCTAGGCT-ATTGTTTTACATTTTTTGTGAGA	336
Db	3372	TAGCTGGGACTACAGG-CATATACCACACCTGGCTAATTTTTTTTGTATTTTGTAGTTGA	3313

RESULT 13
US-10-091-438-77/c
; Sequence 77, Application US/10091438
; Publication No. US20030077606A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ17C1
; CURRENT APPLICATION NUMBER: US/10/091,438
; CURRENT FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 09/764,879
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11

?	PRIOR APPLICATION NUMBER: 50/249,297
?	PRIOR FILING DATE: 2000-11-17
?	PRIOR APPLICATION NUMBER: 50/232,400
?	PRIOR FILING DATE: 2000-09-14
?	PRIOR APPLICATION NUMBER: 50/231,242
?	PRIOR FILING DATE: 2000-09-08
?	PRIOR APPLICATION NUMBER: 50/232,081
?	PRIOR FILING DATE: 2000-09-08
?	PRIOR APPLICATION NUMBER: 50/232,080
?	PRIOR FILING DATE: 2000-09-08
?	PRIOR APPLICATION NUMBER: 50/231,414
?	PRIOR FILING DATE: 2000-09-08
?	PRIOR APPLICATION NUMBER: 50/231,244
?	PRIOR FILING DATE: 2000-09-08
?	PRIOR APPLICATION NUMBER: 50/233,064
?	PRIOR FILING DATE: 2000-09-14
?	PRIOR APPLICATION NUMBER: 50/233,063
?	PRIOR FILING DATE: 2000-09-14
?	PRIOR APPLICATION NUMBER: 50/232,397
?	PRIOR FILING DATE: 2000-09-14
?	PRIOR APPLICATION NUMBER: 50/232,399
?	PRIOR FILING DATE: 2000-09-14
?	PRIOR APPLICATION NUMBER: 50/232,401
?	PRIOR FILING DATE: 2000-09-14
?	PRIOR APPLICATION NUMBER: 50/241,808
?	PRIOR FILING DATE: 2000-10-20
?	PRIOR APPLICATION NUMBER: 50/241,826
?	PRIOR FILING DATE: 2000-10-20
?	PRIOR APPLICATION NUMBER: 50/241,786
?	PRIOR FILING DATE: 2000-10-20
?	PRIOR APPLICATION NUMBER: 50/241,221
?	PRIOR FILING DATE: 2000-10-20
?	PRIOR APPLICATION NUMBER: 50/246,475
?	PRIOR FILING DATE: 2000-11-08
?	PRIOR APPLICATION NUMBER: 50/231,243
?	PRIOR FILING DATE: 2000-09-08

155 TACTCCTTTTCTTTTGTGTTCTCTGTCACCCAGGCTGAAGTACAGTGGTTAGC 214

RESULT 14

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US-09-764-853-209/c
; Sequence 209, Application US/09764853
; Patent No. US20020090672A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, P
; FILE REFERENCES: Fuz06
; CURRENT APPLICATION NUMBER: US/09/76
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - con

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Db 3818 CTGGATTACGGCGTGAGCCACCGCGCGCGCCAGTTAAA 3858

Search completed: June 7, 2003, 23:24:23
Job time : 281 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 7, 2003, 20:36:07 ; Search time 1597 Seconds
(without alignments)
11571.102 Million cell updates/sec

Title: US-09-617-174C-1

Perfect score: 1141

Sequence: 1 agataagcacagcagaag.....aggataactgtgactccagg 1141

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estmu.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: gb_gss.*

18: em_gss_hum.*

19: em_gss_inv.*

20: em_gss_pln.*

21: em_gss_vrt.*

22: em_gss_fun.*

23: em_gss_nam.*

24: em_gss_mus.*

25: em_gss_other.*

26: em_gss_pro.*

27: em_gss_rod.*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	197.8	17.3	496	17 B35967	B35967 HS-1031-A2-
C 2	195	17.1	568	9 AUI59406	AUI59406 AUI59406
C 3	186.2	16.3	410	9 AIO23375	AIO23375 ow63g02.x
C 4	186	16.3	515	14 BM679408	BM679408 UI-E-E00-
C 5	184.2	16.1	708	17 AGI43040	AGI43040 Pan trogl
C 6	184.2	16.1	713	17 AQ312217	AQ312217 RPC111-10

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

7	183.6	16.1	655	17	AGI69306	AGI69306 Pan trogl
8	183	16.0	643	9	AII14719	AII14719 HAI318 Hu
9	183	16.0	2167	11	AF116633	AF116633 Homo sapi
10	182.4	16.0	390	14	R56162	R56162 Y91b06.r1
11	182.4	16.0	742	17	AQ343483	AQ343483 RPC111-12
12	181.8	15.9	649	17	BM609847	BM609847 HVI13C04
13	181.6	15.9	524	10	AW973992	AW973992 EST385990
14	180.6	15.8	571	9	AAI31088	AAI31088 zol6c04.8
15	179.8	15.8	331	12	BG057233	BG057233 7f75d01.x
16	179.8	15.8	661	10	BE177530	BE177530 RCI-HT059
17	179.8	15.8	698	17	AGI41964	AGI41964 Pan trogl
18	179.8	15.8	430	17	AQ393433	AQ393433 CITBI-EI-
19	179.4	15.7	424	9	AI499954	AI499954 t063c10.x
20	179.2	15.7	373	9	AL596605	AL596605 DRF29451C
21	179.2	15.7	531	14	BQ270554	BQ270554 ik05a03.x
22	179.2	15.7	559	12	BG537830	BG537830 602566186
23	179.2	15.7	713	12	BG684208	BG684208 602635838
24	179.2	15.7	893	13	BI913559	BI913559 603180311
25	178.8	15.7	785	14	BM721013	BM721013 UI-E-E00-
26	178.8	15.7	1048	9	AL576528	AL576528 AL576528
27	178.8	15.7	2205	11	AF318346	AF318346 Homo sapi
28	178	15.6	455	17	AQ392348	AQ392348 CITBI-EI-
29	178	15.6	558	17	AQ527359	AQ527359 RPCI-11-3
30	177.8	15.6	279	10	AV754799	AV754799 AV754799
31	177.8	15.6	684	17	AG037064	AG037064 Pan trogl
32	177.6	15.6	430	14	BQ277407	BQ277407 AGENCOURT
33	177.6	15.6	617	14	BQ181121	BQ181121 UI-H-EUO-
34	177.4	15.5	456	9	AI753334	AI753334 cr08f09.x
35	177.4	15.5	512	17	AQ538435	AQ538435 RPCI-11-3
36	177.2	15.5	416	17	AQ748789	AQ748789 HS-5574_A
37	177.2	15.5	515	17	AQ506282	AQ506282 RPCI-11-3
38	177	15.5	532	17	AQ701252	AQ701252 HS-2132.A
39	177	15.5	632	9	AI821267	AI821267 ab9f0f07.x
40	176.6	15.5	562	17	AQ778690	AQ778690 HS-2235.A
41	176.6	15.5	701	17	AGI48726	AGI48726 Pan trogl
42	176.6	15.5	512	17	AQ120174	AQ120174 HS-3028.B
43	176.4	15.5	604	14	BM990713	BM990713 UI-H-D10-
44	176.4	15.5	950	17	AQ749313	AQ749313 HS-5576.A
45	176.2	15.4	471	10	AW151925	AW151925 xf70d02.x

ALIGNMENTS

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LOCUS HS-1031-A2-F07-MR-V0001.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 811 Col=14 Row=K, DNA sequence.
DEFINITION B35967
ACCESSION B35967
VERSION B35967.1 GI:2535336
KEYWORDS GSS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 496)
AUTHORS Mahairas, G.G., Zackrone, K.D., Smith, T., Tipton, S., Schmidt, S., Traicoff, R., Abajian, C., Blanchard, A., West, A. and Hood, L.E.
TITLE Construction of a Characterized Clone Resource for Genomic Sequencing: Generation and Preliminary Analysis of 20,000 Sequence Tagged Connectors
JOURNAL Unpublished (1997)
COMMENT Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 616-8744
Fax: (206) 685-7301
Email: kzackron@u.washington.edu
Sequence Tagged Connector
Plate: CT 811 row: K column: 14
Class: BAC ends
High quality sequence stop: 496.

FEATURES
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 1. .496
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 /db_xref="taxon:9606"
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 /clone_lib="CIT Human Genomic Sperm Library C"
 /sex="M"
 /note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"
BASE COUNT 155 a 85 c 135 g 120 t 1 others
ORIGIN
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 Best Local Similarity 70.3%; Pred. No. 2.5e-29;
 Matches 265; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
 QY 161 TTTTCTTTTGTGTTCTTGTCTCTGTCACCCAGGCTGAAGTACAGTGTAGCTCACGG 220
 Db 487 TCTCTCTTTTTCACGGGGTGTGCTCTGTCTACCCAGGCTGGAGTACAGTGTATGATCACAG 428
 QY 221 CTCACCTGCAGCTTTGACCTCCAGGCTCAAGTACCTCTCGTCTCAGCTTTTCAAGTAA 280
 Db 427 CTCACCTGCAGCTTTGACCTCCAGGCTCAAGTACCTCTCTTCTACCTCAGCCCCCTGAGTAG 368
 QY 281 CTGGGACCAAGCATGTCATCACAGCTAGGCTATTGTTTACATTTTGTAGAGATG 340
 Db 367 CTGGGACCAAGCATGTCATCACAGCTAGGCTATTGTTTACATTTTGTAGAGATG 308
 QY 341 GGGTCTCACATGTTGGCCAGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGC 400
 Db 307 GAGTCTCACTTTGTTGCCAGGCTGGTCTCAAACTCTGAGCTCAAGCAATCCCTCCGCC 248
 QY 401 TCAACCTCCCAATGCTGGGATACAGGCTGAGCCAGCCAGCCAGGCTGAGTAATCC 460
 Db 247 TCAGATCCCAAGTGTGGGATACAGGCTGAGCCAGCCAGCCAGGCTGAGTAATCC 188
 QY 461 TAATCAGAGATTTTAAAGAAACTTCTCGCCCAACCCATTAACAAATATCTCTTACCA 520
 Db 187 CAATATTAGTTTCTCCACCTCCATTCAACAAACACCATCATGCTCATATACCTTGATA 128
 QY 521 ATTGGTAGTAATATT 537
 Db 127 AATGAGAATTTATTATT 111
RESULT 2
AU159406
LOCUS
DEFINITION
 AU159406 THYR01 Homo sapiens cDNA clone THYR01001595 3', mRNA
ACCESSION
 AU159406
VERSION
 AU159406.1 GI:11020927
KEYWORDS
 EST.
SOURCE
 human.
ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
 Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
 Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura, Y., Nagai, T., Sugano
 S. and Isogai, T.).
TITLE
 HRI human cDNA project (Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S.,
 Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Ozawa, M., Nakamura
 Y., Nagai, T., Sugano, S., Isogai, T.)
JOURNAL
 Unpublished (2000)
COMMENT
 Contact: Takao Isogai
 Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.
FEATURES
source
 Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="THYR01001595"
 /clone_lib="THYR01"
 /tissue_type="Chyroid gland"
 /note="Vector: pME18SFL3"
BASE COUNT 141 a 148 c 128 g 142 t 9 others
ORIGIN
 Query Match 17.1%; Score 195; DB 9; Length 568;
 Best Local Similarity 80.6%; Pred. No. 8.5e-29;
 Matches 228; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
 QY 177 TTTTGTCTGTCAACCCAGGCTGAAGTACAGTGTAGTCTCAGGGTCACTGCGAGCTTTGA 236
 Db 13 TCTTGTCTGTCAACCCAGGCTGAAGTGTGAGTGGCAGCATCTGCTCACTGCGAGCTTTGA 72
 QY 237 CTCTCCAGGCTCAAGTATCTCTCTCTCAAGTTTCCAACTGCGGACACAGGCAT 296
 Db 73 CTCTCCAGGCTCAAGTATCTCTCTCCACCTCCGAGTAGCTGGGACTACAGGCAT 132
 QY 297 GCATCACCAAGCTAGGCTATTGTTTACATTTTGTAGAGATGGGCTCACCAGTTG 356
 Db 133 GCACCAACCAAGCTAGGCTATTGTTTGTACTTTTGTAGAGAGGGGTTTACCAGTTG 192
 QY 357 CCCAGGTGCTCTCAAACTCTCTGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAAAATG 416
 Db 193 CACAGGCTGTCTCAGACTCTCTGGGCTCAAGCTATCCGCTGCTTGGGCTCCCAAGTG 252
 QY 417 CTGGGATTACAGCGGTGAGCCACCGGGCCAGGGCTGAGTAATC 459
 Db 253 CTGGGATTACAACTGGGAGCCACCGTGGCCGCGGAGATCTC 295
RESULT 3
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LOCUS
DEFINITION
 AI023375.1 GI:3239781
 AI023375 410 bp mRNA linear EST 28-AUG-1998
 ow63g02.xl Soares senescent fibroblasts NBHSF Homo sapiens cDNA
 clone IMAGE:1651538 3' similar to contains Alu repetitive element;;
ACCESSION
 AI023375
VERSION
 AI023375.1
KEYWORDS
 EST.
SOURCE
 human.
ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
JOURNAL
 Unpublished (1997)
COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 Insert Length: 1166 Std Error: 0.00
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 335.
FEATURES
source
 Location/Qualifiers
 1. .410
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 /db_xref="taxon:9606"
 /clone="IMAGE:1651538"
 /clone_lib="Soares senescent fibroblasts_NBHSF"
 /tissue_type="senescent fibroblast"
 /lab_host="DH10B (ampicillin resistant)"
 /note="Vector: pT7T3D (Pharmacia) with a modified

polylinker V-TYPE: phagemid; Site_1: Not I; Site_2: Eco RI
; 1st strand cDNA was primed with a Not I - oligo(dT)
primer [5']
TGTACCAATCTGAAGTGGAGCGCGCATTTTTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by Bento
Soares and M.Fatima Bonaldo."
BASE COUNT 126 a 85 c 112 g 87 t
ORIGIN

Query Match 16.3%; Score 186.2; DB 9; Length 410;
Best Local Similarity 70.7%; Pred. No. 5.1e-27;
Matches 248; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 142 GAGCAGAGCTGGTACTCTCTTTCTTTTGTCTTTCTGTCACCGAGGTGAG 201
DB 409 GGGCTGGCTCATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 350
QY 202 TACAGTGGTGTAGCTCAGGCTCACTGACGCTTGTACCTCCAGGCTCAAGTATCTCTC 261
DB 349 TCGAGTGGTATGATCTGGCTCACTGCACTCTCCAGGCTCAAGGATCTCTCC 290
QY 262 GTCTCAGCTTCCAGTAACTGGGACACAGGATGATCACCAGCTAGGCTATTGTTT 321
DB 289 AACTCAGCTCCCAAGTAGCTGGACTACAGGTACATGCCACACACCTGGCTGTTTC 230
QY 322 TACATTTTTGTAGAGATGGGTCTCACCATGTGGCCAGGTTGGTCTCAAACTCTGGG 381
DB 229 TGTATTTTTAGTAGAGTGGGTTTCCACCATGTGGCCAGGCTGGTCTTGAACCTCTGAG 170
QY 382 CTCAAGCAATCCGCTCACGCTCAACCTCCCAATGCTGGATTACAGGCTGAGCACCG 441
DB 169 CTCAGTATCACCCTGCTTGGCTCCCAAGTCTGGATTACAGGCTGAGCACCA 110
QY 442 GGCAGGCTGAGTAACTTAATCAGAGGATTTTAAAGAAACTTCCTGC 492
DB 109 TGCCAGCGAATGATTCATTTTCACTGCTGCTGTGTAGTGACTTC 59

RESULT 4
BM679408
LOCUS
DEFINITION
UI-B-E00-ahz-1-04-0-UI.81 UI-E-E00 Homo sapiens cDNA clone
UI-B-E00-ahz-1-04-0-UI 3', mRNA sequence.
BM679408
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 515)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
9704477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).

The following repetitive elements were found in this cDNA
sequence: 12-302, >ALU (matched complement)
Seq primer: M13 Forward
POLVA=Yes.

FEATURES

Location/Qualifiers
1..515
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/db_xref="taxon:9606"
/clone="UI-B-E00-ahz-1-04-0-UI"
/clone_lib="UI-E-E00"
/tissue type="fetal eye"
/dev stage="fetal"
/lab_host="DH10B (Life Technologies) (T1 phage resistant)"
/note="Organ: eye; Vector: pT73-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-B-E00 is a cDNA library containing the following
tissue(s): fetal eye. The library was constructed
according to Bonaldo, Lennon and Soares, Genome Research,
6:791-806, 1996. First strand cDNA synthesis was primed
with an oligo-dT primer containing a Not I site. Double
stranded cDNA was ligated to an EcoR I adaptor, digested
with Not I, and cloned directionally into pT73-Pac
vector. The oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CCGGTATACC. This library
was created for the program, Gene Discovery in the Visual
System, supported by National Eye Institute (NEI).
TAG_LIB=UI-E-E00
TAG_TISSUE=human fetal eye
TAG_SEQ=CGGTATACC"

BASE COUNT 130 a 126 c 100 g 157 t 2 others
ORIGIN

Query Match 16.3%; Score 186; DB 14; Length 515;
Best Local Similarity 79.9%; Pred. No. 5.3e-27;
Matches 219; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 180 TGCTCTGTCAACCCAGGCTGAAGTACAGTGGTTAGTCTCAGCGTCACTGAGCTTTGACCT 239
DB 32 TGGTCTGCCACCCAGGCTGGAGTGCAGTGGCATGATCCAGCTCACTGAGCTTGACCT 91
QY 240 CCCAGGCTCAAGTATCTCTCTGCTCAGCTTTTCAAGTAACTGGGACACAGGATGCA 299
DB 92 CCAGGCTCAGGGATCTTACCACCTCAGCTTCCAGGTAGCTGGAACACAGGATGG 151
QY 300 TCACCAGCTAGGCTATTGTTTACATTTTGTAGATGGGTCTCACCATTGTCCT 359
DB 152 CCACCATGCTGGCTAATTTTTCGTATTTTGTAGACAGGGTTTTGCCTATGTCCT 211
QY 360 AGTTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAGCTCAACCTCCCAAAATGCTG 419
DB 212 AGGCTGGTCTCAATTTCTGGCTCAAGCAATCTGCCACCTCAGCTTCCCAAAATGCTG 271
QY 420 GGATTACAGGCTGAGCCAGCGGCGCAGGCTGA 453
DB 272 GGATTACAGGCTGAGCCAGCGCAGCGCTGA 305

RESULT 5
AG143040/c
LOCUS
DEFINITION
Pan troglodytes DNA, clone: RP43-003J20.TJ, genomic survey
sequence.
AG143040
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Pan troglodytes male lymphocytes DNA, clone: RP43-003J20.TJ.
Male BAC Library clone: RP43-003J20.TJ.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
1

ORGANISM

[illegible]

TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
JOURNAL Map Building
COMMENT Unpublished (1997)
 Contact: Shaying Zhao, William Nierman, Mark Adams
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: hbeetigr.org
 Clones are derived from the human BAC library RPCI-11. For BAC
 library availability, please contact Pieter de Jong
 (pieterdejong.med.buffalo.edu). Clones may be purchased from
 BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from
 Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tcdb/humgen/bac_end_search/bac_end_search.html
 Seq primer: SP6
 Class: BAC ends.

FEATURES

source

Location/Qualifiers

1. .742
 /organism="Homo sapiens"
 /db_xref="GDB:7546761"
 /db_xref="taxon:9606"
 /clone="RPCI-11-122M10"
 /clone_lib="RPCI-11"
 /sex="Male"
 /cell_type="Lymphocytes"
 /notes="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
 RPCI11 Human Male BAC Library"
 BASE COUNT 231 a 141 c 146 g 224 t
 ORIGIN

Query Match 16.0%; Score 182.4; DB 17; Length 742;
 Best Local Similarity 75.0%; Pred. No. 2.5e-26;
 Matches 228; Conservative 0; Mismatches 76; Indels 0; Gaps 0;
 QY 161 TTTTCTTTTGTCTCTGTGCTCCAGGCTGAAGTACAGTGGTTAGCTCACGG 220
 |||||
 DB 231 TTTTGTGATACAGGGTTTCACTCTGTCCAGGCTGGAGTACAGTAGTGAACATGG 230
 QY 221 CTCAGTCGAGCTTGGACCTCCAGGCTCAAGTATCTCTGCTCAGCTTCCAGTAA 280
 |||||
 DB 291 CTGACTGCAGCTTGACCTCTGACTCAGGTGATCTCCGCTCAGCCTCCCAAGTAG 350
 QY 281 CTGGGACCAAGCATGATCACCAGCTAGGCTATTGTTTACATTTTGTAGAGATG 340
 |||||
 DB 351 CTGGGACTACAGTGTGACCAACCTTGTCTAAATTTTGTATTTTTGTAGAGACG 410
 QY 341 GGGTCTCACCATGTTGCCAGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAG 400
 |||||
 DB 411 GGTGTTTGCCATGTTGCCAGGCTGGTTTCAAAATCTGGGCTCAAGCAATCTCTGTC 470
 QY 401 TCAACTTCCCAATAGCTGGGATACAGGCTGAGCACCAGGCTGAGTATCC 460
 |||||
 DB 471 TTGGCTCTCCCTAAGTTCTGAGATACAAAGTGTGAGCCAGCGCTGGCTGTTGTATA 530
 QY 461 TAAT 464
 |||||
 DB 531 TACT 534

RESULT 12
BH609847/c
LOCUS BH609847 649 bp DNA linear GSS 18-DEC-2001
DEFINITION HIV13C04 SupT1 HIV-1 in vivo integration lines Homo sapiens genomic
 Clone HIV13C04, DNA sequence.
ACCESSION BH609847
VERSION BH609847.1 GI:17922456
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE
AUTHORS

TITLE
JOURNAL
COMMENT

Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
 1 (bases 1 to 649)
 Schroder,A.R.W., Shinn,P., Chen,H., Berry, C., Ecker,J.R. and
 Bushman,P.
 Favored Sites for HIV-1 Integration in the Human Genome
 Unpublished (2002)
 Contact: Frederic Bushman
 Salk Institute Infectious Disease Laboratory
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1630
 Fax: 858 554 0341
 Email: bushman@salk.edu
 Class: PCR with specific primers.
 Location/Qualifiers

1. .649
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="HIV13C04"
 /cell_line="SupT1"
 /note="A human T-cell line (SupT1) was infected with an
 HIV-based vector. DNA was isolated and cleaved with
 restriction enzymes; linkers were ligated onto the cleaved
 DNA and DNAs were amplified using one primer that bound to
 the linker DNA and one that bound to the HIV cDNA.
 Junctions between integrated HIV proviruses and cellular
 DNA were cloned and sequenced."
 BASE COUNT 228 a 88 c 170 g 163 t
 ORIGIN

Query Match 15.9%; Score 181.8; DB 17; Length 649;
 Best Local Similarity 77.9%; Pred. No. 3.4e-26;
 Matches 219; Conservative 0; Mismatches 62; Indels 0; Gaps 0;
 QY 161 TTTTCTTTTGTCTCTGTGCTCCAGGCTGAAGTACAGTGGTTAGCTCACGG 220
 |||||
 DB 305 TTTTCTTTTGTAGATCTCACTCTGTCCAGGCTGCAGTGCAGTGGCGGATCTCAG 246
 QY 221 CTCAGTCGAGCTTGGACCTCCAGGCTCAAGTATCTCTGCTCAGCTTCCAAAGTAA 280
 |||||
 DB 245 CTCAGTCAACCTTCCACCTCCAGGTTCAAGTATCTCTGCTCAGCCTCCCAAGTAG 186
 QY 281 CTGGGACCAAGCATGATCACCAGCTAGGCTATTGTTTACATTTTGTAGAGATG 340
 |||||
 DB 185 CTGGGACTACAGGCACACACACCGCTGCTAATTTTGTATTTTTGTAGAGACA 126
 QY 341 GGGTCTCACCATGTTGCCAGGTTGGTCTCAAACTCTGGGCTCAAGCAATCCGCTCAG 400
 |||||
 DB 125 GGGTCTCACCATGTTGCCAGTCTGCTCTCAAACTCTAACTCAGGTGATCTGCCACC 66
 QY 401 TCAACCTCCCAATAGCTGGGATACAGGCTGAGCCAGCG 441
 |||||
 DB 65 TCAGCCTCCAGAGTCTAGGATTACAGGTGTGAGCCACCG 25

RESULT 13
AW973992
LOCUS AW973992 524 bp mRNA linear EST 02-JUN-2000
DEFINITION EST385990 MAGE resequences, MAGM Homo sapiens cDNA, mRNA sequence.
ACCESSION AW973992
VERSION AW973992.1 GI:8165076
KEYWORDS EST.
SOURCE human.

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 524)
AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
 I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
 Quackenbush,J.
 Assessment of gene expression patterns in a model of colon tumor
 metastasis using a 19,200 element cDNA microarray

found through the I.M.A.G.E. Consortium/LLNL at:

info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 312.

FEATURES

source

Location/Qualifiers
1. .331
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3302809"
/clone_lib="Lupski_dorsal_root_ganglion"
/sex="male"
/tissue type="dorsal root ganglia"
/dev stage="adult, 36 yr"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1:
NotI; Site_2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
5'-GACTAGTTCTAGATCGGAGCGGCCCTT(15)-3'. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

BASE COUNT 78 a 88 c 73 g 92 t

ORIGIN

Query Match 15.8%; Score 179.8; DB 12; Length 331;
Best Local Similarity 76.7%; Pred. No. 1e-25;
Matches 220; Conservative 0; Mismatches 67; Indels 0; Gaps 0;
QY 177 TTTTGTCTGTCAACCAGGCTGAAGTACAGTGGTTAGTCAACGGCTCAGTGCAGCTTTGA 236
DB 12 TCTCACTCTGTCAACCAGGCTGGAGTACGGTGTATGATCAGAGCTCACTGCAGCCTCTA 71
QY 237 CCTCCAGGCTCAAGTGATCCTCTCGTCTCAGCTTTCCAGTAACTGGGACACACAGCAT 296
DB 72 CCTTCCAGGCTCAAGTGATCCTCTCACTTCAAGCTCCCTTGTAGCTGGGACCAACAGGTGC 131
QY 297 GCATCACACGCTAGGCTATTGTTTACATTTTGTAGAGATGGGTCTCACCATGTTG 356
DB 132 GTGCCACACACTTGGCTAATTTTAAATTTTGTAGAGATGGGTCTTGTATGTTG 191
QY 357 CCCAGTTGGTCTCAAACTCCTGGGCTCAAGCAATCGGCTCAGCTCAACCTCCCAAATG 416
DB 192 CCCAGGCTGTCTCAAACTCCTGGGCTCAAGTGCTTTTGGCTCAGCTCCCAAAGTG 251
QY 417 CTGGGATTACAGCGGTGACCCAGGCGCCAGGCTGAGTAATCCTAA 463
DB 252 CTGGGACTACAGCATGAGCTACTGCGCCCGAGCCTTAGAAACTTTA 298

Search completed: June 7, 2003, 22:23:20
Job time : 1604 secs

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